

# SEQUENCE LISTING

<110> McMullin, Thomas  
Ding, Ming-De  
Grund, Alan

<120> Metabolic Engineering for Enhanced Production of Chitin and  
Chitosan in Microorganisms

<130> 3161-18-3

<150> 60/462,087

<151> 2003-04-11

<160> 59

<170> PatentIn version 3.2

<210> 1  
<211> 32  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 1  
agctgagctc atgtgtggaa ttgttggcgc ga

32

<210> 2  
<211> 32  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 2  
tacgaagctt actcaaccgt aaccgatttt gc

32

<210> 3  
<211> 25  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 3  
ggcggccgct ctagccaggt ctccc

25

<210> 4  
<211> 41  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 4  
ggagctccac cgcggtggcg gccgctctag ccaggtctcc c

41

<210> 5  
<211> 38  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> primer  
  
<400> 5  
atgcggattc atgtgtggaa tcgtaggtta tatccctc 38

<210> 6  
<211> 38  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> primer  
  
<400> 6  
gatcctcgag ttactccaca gtaacactct tcgcaagg 38

<210> 7  
<211> 34  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> primer  
  
<400> 7  
aggcgaattc atgtgtggta tctttgggta ctgc 34

<210> 8  
<211> 34  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> primer  
  
<400> 8  
aggcctgcag ttattcgacg gtaacagatt tagc 34

<210> 9  
<211> 36  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> primer  
  
<400> 9  
cctgcagccc gggggatccg cccggatcgg tctcgc 36

<210> 10  
<211> 32

<212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 10  
 gatccgccccg atcgaattca gcatgagctt ac 32  
  
  
 <210> 11  
 <211> 35  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 11  
 gattacgccca agcgcgcaat taaccctcac taaag 35  
  
  
 <210> 12  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 12  
 gcatgcggcc gcttcgtcgc ctaatgtctc g 31  
  
  
 <210> 13  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 13  
 gcatctcgag cccggtgtct gtatttccgg 30  
  
  
 <210> 14  
 <211> 29  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 14  
 gcatcctcag catgtgtgga attgttggc 29  
  
  
 <210> 15  
 <211> 27  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer  
  
 <400> 15  
 gcatgtcgac ttactcaacc gtaaccg 27  
  
 <210> 16  
 <211> 36  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 16  
 agctcctcag caatgtgtgg tatctttggt tactgc 36  
  
 <210> 17  
 <211> 34  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 17  
 aggcctcgag ttattcgacg gtaacagatt tagc 34  
  
 <210> 18  
 <211> 43  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 18  
 gcgggggcct cagcaatgaa aattttcaat acaatacaat ctg 43  
  
 <210> 19  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 19  
 gcgggggtcg acctagtcgt agcgttcgat g 31  
  
 <210> 20  
 <211> 44  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer

<400> 20  
 gcggggcctc agcaatgaga atacaactaa atacaattga tttg 44

<210> 21  
 <211> 44  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 21  
 cttcaattcc cgtcgactta ggacaagaat tcttttatgt aatc 44

<210> 22  
 <211> 1830  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (1)..(1830)

<400> 22  
 atg tgt gga att gtt ggc gcg atc gcg caa cgt gat gta gca gaa atc 48  
 Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile  
 1 5 10 15  
 ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96  
 Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala  
 20 25 30  
 ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144  
 Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg  
 35 40 45  
 ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192  
 Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu  
 50 55 60  
 cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240  
 His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu  
 65 70 75 80  
 cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg 288  
 Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val  
 85 90 95  
 gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta 336  
 Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu  
 100 105 110  
 aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att 384  
 Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile  
 115 120 125  
 gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag 432  
 Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu  
 130 135 140

gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val 145 150 155 160	480
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly 165 170 175	528
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser 180 185 190	576
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu 275 280 285	864
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser 290 295 300	912
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly 305 310 315 320	960
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser 325 330 335	1008
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu 340 345 350	1056
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr 355 360 365	1104
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg 370 375 380	1152
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val 1200	1200

385	390	395	400	
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg				1248
Ala Ser Thr Lys	Ala Phe Thr Thr	Gln Leu Thr	Val Leu Leu Met Leu	
	405	410	415	
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat				1296
Val Ala Lys	Leu Ser Arg Leu Lys	Gly Leu Asp Ala	Ser Ile Glu His	
	420	425	430	
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg				1344
Asp Ile Val His	Gly Leu Gln Ala	Leu Pro Ser Arg	Ile Glu Gln Met	
	435	440	445	
ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac				1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu		Ala Glu Asp Phe Ser Asp		
	450	455	460	
aaa cat cac gcg ctg ttc ctg ggc cgt ggc gat cag tac cca atc gcg				1440
Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala				
	465	470	475	480
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa				1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu				
	485	490	495	
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat				1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp				
	500	505	510	
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa				1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu				
	515	520	525	
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg				1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu				
	530	535	540	
tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg				1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met				
	545	550	555	560
cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc				1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe				
	565	570	575	
tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa				1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys				
	580	585	590	
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt				1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val				
	595	600	605	
gag taa				1830
Glu				

<210> 23  
 <211> 609  
 <212> PRT

<213> Escherichia coli

<400> 23

Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile  
1 5 10 15

Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala  
20 25 30

Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg  
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu  
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu  
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val  
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu  
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile  
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu  
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val  
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly  
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser  
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu  
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp  
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln  
225 230 235 240



Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu  
 245 250 255  
 Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile  
 260 265 270  
 Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu  
 275 280 285  
 Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser  
 290 295 300  
 Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly  
 305 310 315 320  
 Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser  
 325 330 335  
 Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu  
 340 345 350  
 Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr  
 355 360 365  
 Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg  
 370 375 380  
 Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val  
 385 390 395 400  
 Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu  
 405 410 415  
 Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His  
 420 425 430  
 Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met  
 435 440 445  
 Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp  
 450 455 460  
 Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala  
 465 470 475 480  
 Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu

485										490					495				
Ala	Tyr	Ala	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Ile	Asp				
			500					505					510						
Ala	Asp	Met	Pro	Val	Ile	Val	Val	Ala	Pro	Asn	Asn	Glu	Leu	Leu	Glu				
		515					520					525							
Lys	Leu	Lys	Ser	Asn	Ile	Glu	Glu	Val	Arg	Ala	Arg	Gly	Gly	Gln	Leu				
	530					535					540								
Tyr	Val	Phe	Ala	Asp	Gln	Asp	Ala	Gly	Phe	Val	Ser	Ser	Asp	Asn	Met				
545					550				555						560				
His	Ile	Ile	Glu	Met	Pro	His	Val	Glu	Glu	Val	Ile	Ala	Pro	Ile	Phe				
				565					570					575					
Tyr	Thr	Val	Pro	Leu	Gln	Leu	Leu	Ala	Tyr	His	Val	Ala	Leu	Ile	Lys				
			580					585					590						
Gly	Thr	Asp	Val	Asp	Gln	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val				
		595					600					605							

Glu

<210> 24  
 <211> 1830  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (1)..(1830)

<400> 24	
atg tgt gga att gtt ggc gcg atc gcg caa cgt gat gta gca gaa atc	48
Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile	
1 5 10 15	
ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc	96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala	
20 25 30	
ggt ctg gcc gtt gtt gat aca gaa ggt cat atg acc cgc ctg cgt cgc	144
Gly Leu Ala Val Val Asp Thr Glu Gly His Met Thr Arg Leu Arg Arg	
35 40 45	
ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg	192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu	
50 55 60	

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu 65 70 75 80	240
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val 85 90 95	288
gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu 100 105 110	336
aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile 115 120 125	384
gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu 130 135 140	432
gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val 145 150 155 160	480
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly 165 170 175	528
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser 180 185 190	576
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac tgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu 275 280 285	864
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser 290 295 300	912
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly	960

305		310		315		320	
att ccg tgc gac gtc gaa atc gcc tcc gaa ttc cgc tat cgc aaa tct							1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser		325		330		335	
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa							1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu		340		345		350	
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac							1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr		355		360		365	
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc							1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg		370		375		380	
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg							1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val		385		390		400	
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg							1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu		405		410		415	
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat							1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His		420		425		430	
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg							1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met		435		440		445	
ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac							1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp		450		455		460	
aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg							1440
Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala		465		470		475	480
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa							1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu		485		490		495	
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat							1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp		500		505		510	
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa							1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu		515		520		525	
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg							1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu		530		535		540	
tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg							1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met		545		550		555	560

cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc	1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe	
565 570 575	
tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa	1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys	
580 585 590	
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt	1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val	
595 600 605	
gag taa	1830
Glu	

<210> 25  
 <211> 609  
 <212> PRT  
 <213> Escherichia coli

<400> 25

Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile	
1 5 10 15	
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala	
20 25 30	
Gly Leu Ala Val Val Asp Thr Glu Gly His Met Thr Arg Leu Arg Arg	
35 40 45	
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu	
50 55 60	
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu	
65 70 75 80	
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val	
85 90 95	
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu	
100 105 110	
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile	
115 120 125	
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu	
130 135 140	
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val	
145 150 155 160	

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly  
 165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser  
 180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu  
 195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp  
 210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln  
 225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu  
 245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile  
 260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu  
 275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser  
 290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly  
 305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser  
 325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu  
 340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr  
 355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg  
 370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val  
 385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu

				405					410					415	
Val	Ala	Lys	Leu	Ser	Arg	Leu	Lys	Gly	Leu	Asp	Ala	Ser	Ile	Glu	His
			420					425					430		
Asp	Ile	Val	His	Gly	Leu	Gln	Ala	Leu	Pro	Ser	Arg	Ile	Glu	Gln	Met
		435					440					445			
Leu	Ser	Gln	Asp	Lys	Arg	Ile	Glu	Ala	Leu	Ala	Glu	Asp	Phe	Ser	Asp
	450					455					460				
Lys	His	His	Ala	Leu	Phe	Leu	Ser	Arg	Gly	Asp	Gln	Tyr	Pro	Ile	Ala
465					470					475					480
Leu	Glu	Gly	Ala	Leu	Lys	Leu	Lys	Glu	Ile	Ser	Tyr	Ile	His	Ala	Glu
				485					490					495	
Ala	Tyr	Ala	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Ile	Asp
			500					505					510		
Ala	Asp	Met	Pro	Val	Ile	Val	Val	Ala	Pro	Asn	Asn	Glu	Leu	Leu	Glu
		515					520					525			
Lys	Leu	Lys	Ser	Asn	Ile	Glu	Glu	Val	Arg	Ala	Arg	Gly	Gly	Gln	Leu
	530					535					540				
Tyr	Val	Phe	Ala	Asp	Gln	Asp	Ala	Gly	Phe	Val	Ser	Ser	Asp	Asn	Met
545					550					555					560
His	Ile	Ile	Glu	Met	Pro	His	Val	Glu	Glu	Val	Ile	Ala	Pro	Ile	Phe
				565					570					575	
Tyr	Thr	Val	Pro	Leu	Gln	Leu	Leu	Ala	Tyr	His	Val	Ala	Leu	Ile	Lys
			580					585					590		
Gly	Thr	Asp	Val	Asp	Gln	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val
		595					600					605			

Glu

```
<210> 26
<211> 1803
<212> DNA
<213> Bacillus subtilis
```

<220>

<221> CDS  
 <222> (1)..(1803)

<400> 26  
 atg tgt gga atc gta ggt tat atc ggt cag ctt gat gcg aag gaa att 48  
 Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Leu Asp Ala Lys Glu Ile  
 1 5 10 15

tta tta aaa ggg tta gag aag ctt gag tat cgc ggt tat gac tct gct 96  
 Leu Leu Lys Gly Leu Glu Lys Leu Glu Tyr Arg Gly Tyr Asp Ser Ala  
 20 25 30

ggt att gct gtt gcc aac gaa cag gga atc cat gtg ttc aaa gaa aaa 144  
 Gly Ile Ala Val Ala Asn Glu Gln Gly Ile His Val Phe Lys Glu Lys  
 35 40 45

gga cgc att gca gat ctt cgt gaa gtt gtg gat gcc aat gta gaa gcg 192  
 Gly Arg Ile Ala Asp Leu Arg Glu Val Val Asp Ala Asn Val Glu Ala  
 50 55 60

aaa gcc gga att ggg cat act cgc tgg gcg aca cac ggc gaa cca agc 240  
 Lys Ala Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Glu Pro Ser  
 65 70 75 80

tat ctg aac gct cac ccg cat caa agc gca ctg ggc cgc ttt aca ctt 288  
 Tyr Leu Asn Ala His Pro His Gln Ser Ala Leu Gly Arg Phe Thr Leu  
 85 90 95

gtt cac aac ggc gtg atc gag aac tat gtt cag ctg aag caa gag tat 336  
 Val His Asn Gly Val Ile Glu Asn Tyr Val Gln Leu Lys Gln Glu Tyr  
 100 105 110

ttg caa gat gta gag ctc aaa agt gac acc gat aca gaa gta gtc gtt 384  
 Leu Gln Asp Val Glu Leu Lys Ser Asp Thr Asp Thr Glu Val Val Val  
 115 120 125

caa gta atc gag caa ttc gtc aat gga gga ctt gag aca gaa gaa gcg 432  
 Gln Val Ile Glu Gln Phe Val Asn Gly Gly Leu Thr Glu Thr Glu Ala  
 130 135 140

ttc cgc aaa aca ctt aca ctg tta aaa ggc tct tat gca att gct tta 480  
 Phe Arg Lys Thr Leu Thr Leu Leu Lys Gly Ser Tyr Ala Ile Ala Leu  
 145 150 155 160

ttc gat aac gac aac aga gaa acg att ttt gta gcg aaa aac aaa agc 528  
 Phe Asp Asn Asp Asn Arg Glu Thr Ile Phe Val Ala Lys Asn Lys Ser  
 165 170 175

cct cta tta gta ggt ctt gga gat aca ttc aac gtc gta gca tct gat 576  
 Pro Leu Leu Val Gly Leu Gly Asp Thr Phe Asn Val Val Ala Ser Asp  
 180 185 190

gcg atg gcg atg ctt caa gta acc aac gaa tac gta gag ctg atg gat 624  
 Ala Met Ala Met Leu Gln Val Thr Asn Glu Tyr Val Glu Leu Met Asp  
 195 200 205

aaa gaa atg gtt atc gtc act gat gac caa gtt gtc atc aaa aac ctt 672  
 Lys Glu Met Val Ile Val Thr Asp Asp Gln Val Val Ile Lys Asn Leu  
 210 215 220

gat ggt gac gtg att aca cgt gcg tct tat att gct gag ctt gat gcc 720  
 Asp Gly Asp Val Ile Thr Arg Ala Ser Tyr Ile Ala Glu Leu Asp Ala



225		230		235		240	
agt gat atc gaa aaa ggc acg tac cct cac tac atg ttg aaa gaa acg							768
Ser Asp Ile Glu Lys Gly Thr Tyr Pro His Tyr Met Leu Lys Glu Thr							
		245		250		255	
gat gag cag cct gtt gtt atg cgc aaa atc atc caa acg tat caa gat							816
Asp Glu Gln Pro Val Val Met Arg Lys Ile Ile Gln Thr Tyr Gln Asp							
		260		265		270	
gaa aac ggc aag ctg tct gtg cct ggc gat atc gct gcc gct gta gcg							864
Glu Asn Gly Lys Leu Ser Val Pro Gly Asp Ile Ala Ala Ala Val Ala							
		275		280		285	
gaa gcg gac cgc atc tat atc att ggc tgc gga aca agc tac cat gca							912
Glu Ala Asp Arg Ile Tyr Ile Ile Gly Cys Gly Thr Ser Tyr His Ala							
		290		295		300	
gga ctt gtc ggt aaa caa tat att gaa atg tgg gca aac gtg ccg gtt							960
Gly Leu Val Gly Lys Gln Tyr Ile Glu Met Trp Ala Asn Val Pro Val							
		305		310		315	320
gaa gtg cat gta gcg agt gaa ttc tcc tac aac atg ccg ctt ctg tct							1008
Glu Val His Val Ala Ser Glu Phe Ser Tyr Asn Met Pro Leu Leu Ser							
		325		330		335	
aag aaa ccg ctc ttc att ttc ctt tct caa agc gga gaa aca gca gac							1056
Lys Lys Pro Leu Phe Ile Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp							
		340		345		350	
agc cgc gcg gta ctc gtt caa gtc aaa gcg ctc gga cac aaa gcc ctg							1104
Ser Arg Ala Val Leu Val Gln Val Lys Ala Leu Gly His Lys Ala Leu							
		355		360		365	
aca atc aca aac gta cct gga tca acg ctt tct cgt gaa gct gac tat							1152
Thr Ile Thr Asn Val Pro Gly Ser Thr Leu Ser Arg Glu Ala Asp Tyr							
		370		375		380	
aca ttg ctg ctt cat gca ggc cct gag atc gct gtt gcg tca acg aaa							1200
Thr Leu Leu Leu His Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys							
		385		390		395	400
gca tac act gca caa atc gca gtt ctg gcg gtt ctt gct tct gtg gct							1248
Ala Tyr Thr Ala Gln Ile Ala Val Leu Ala Val Leu Ala Ser Val Ala							
		405		410		415	
gct gac aaa aat ggc atc aat atc gga ttt gac ctc gtc aaa gaa ctc							1296
Ala Asp Lys Asn Gly Ile Asn Ile Gly Phe Asp Leu Val Lys Glu Leu							
		420		425		430	
ggt atc gct gca aac gca atg gaa gct cta tgc gac cag aaa gac gaa							1344
Gly Ile Ala Ala Asn Ala Met Glu Ala Leu Cys Asp Gln Lys Asp Glu							
		435		440		445	
atg gaa atg atc gct cgt gaa tac ctg act gta tcc aga aat gct ttc							1392
Met Glu Met Ile Ala Arg Glu Tyr Leu Thr Val Ser Arg Asn Ala Phe							
		450		455		460	
ttc atc gga cgc ggc ctt gac tac ttc gta tgt gtc gaa ggc gca ctg							1440
Phe Ile Gly Arg Gly Leu Asp Tyr Phe Val Cys Val Glu Gly Ala Leu							
		465		470		475	480

aag ctg aaa gag att tct tac atc cag gca gaa ggt ttt gcc ggc ggt	1488
Lys Leu Lys Glu Ile Ser Tyr Ile Gln Ala Glu Gly Phe Ala Gly Gly	
485 490 495	
gag cta aag cac gga acg att gcc ttg atc gaa caa gga aca cca gta	1536
Glu Leu Lys His Gly Thr Ile Ala Leu Ile Glu Gln Gly Thr Pro Val	
500 505 510	
ttc gca ctg gca act caa gag cat gta aac cta agc atc cgc gga aac	1584
Phe Ala Leu Ala Thr Gln Glu His Val Asn Leu Ser Ile Arg Gly Asn	
515 520 525	
gtc aaa gaa gtt gct gct cgc gga gca aac aca tgc atc atc tca ctg	1632
Val Lys Glu Val Ala Ala Arg Gly Ala Asn Thr Cys Ile Ile Ser Leu	
530 535 540	
aaa ggc cta gac gat gcg gat gac aga ttc gta ttg ccg gaa gta aac	1680
Lys Gly Leu Asp Asp Ala Asp Asp Arg Phe Val Leu Pro Glu Val Asn	
545 550 555 560	
cca gcg ctt gct ccg ttg gta tct gtt gtt cca ttg cag ctg atc gct	1728
Pro Ala Leu Ala Pro Leu Val Ser Val Val Pro Leu Gln Leu Ile Ala	
565 570 575	
tac tat gct gca ctg cat cgc ggc tgt gat gtg gat aaa cct cgt aac	1776
Tyr Tyr Ala Ala Leu His Arg Gly Cys Asp Val Asp Lys Pro Arg Asn	
580 585 590	
ctt gcg aag agt gtt act gtg gag taa	1803
Leu Ala Lys Ser Val Thr Val Glu	
595 600	

<210> 27  
 <211> 600  
 <212> PRT  
 <213> Bacillus subtilis

<400> 27

Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Leu Asp Ala Lys Glu Ile	
1 5 10 15	
Leu Leu Lys Gly Leu Glu Lys Leu Glu Tyr Arg Gly Tyr Asp Ser Ala	
20 25 30	
Gly Ile Ala Val Ala Asn Glu Gln Gly Ile His Val Phe Lys Glu Lys	
35 40 45	
Gly Arg Ile Ala Asp Leu Arg Glu Val Val Asp Ala Asn Val Glu Ala	
50 55 60	
Lys Ala Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Glu Pro Ser	
65 70 75 80	
Tyr Leu Asn Ala His Pro His Gln Ser Ala Leu Gly Arg Phe Thr Leu	
85 90 95	

Val His Asn Gly Val Ile Glu Asn Tyr Val Gln Leu Lys Gln Glu Tyr  
 100 105 110

Leu Gln Asp Val Glu Leu Lys Ser Asp Thr Asp Thr Glu Val Val Val  
 115 120 125

Gln Val Ile Glu Gln Phe Val Asn Gly Gly Leu Glu Thr Glu Glu Ala  
 130 135 140

Phe Arg Lys Thr Leu Thr Leu Leu Lys Gly Ser Tyr Ala Ile Ala Leu  
 145 150 155 160

Phe Asp Asn Asp Asn Arg Glu Thr Ile Phe Val Ala Lys Asn Lys Ser  
 165 170 175

Pro Leu Leu Val Gly Leu Gly Asp Thr Phe Asn Val Val Ala Ser Asp  
 180 185 190

Ala Met Ala Met Leu Gln Val Thr Asn Glu Tyr Val Glu Leu Met Asp  
 195 200 205

Lys Glu Met Val Ile Val Thr Asp Asp Gln Val Val Ile Lys Asn Leu  
 210 215 220

Asp Gly Asp Val Ile Thr Arg Ala Ser Tyr Ile Ala Glu Leu Asp Ala  
 225 230 235 240

Ser Asp Ile Glu Lys Gly Thr Tyr Pro His Tyr Met Leu Lys Glu Thr  
 245 250 255

Asp Glu Gln Pro Val Val Met Arg Lys Ile Ile Gln Thr Tyr Gln Asp  
 260 265 270

Glu Asn Gly Lys Leu Ser Val Pro Gly Asp Ile Ala Ala Ala Val Ala  
 275 280 285

Glu Ala Asp Arg Ile Tyr Ile Ile Gly Cys Gly Thr Ser Tyr His Ala  
 290 295 300

Gly Leu Val Gly Lys Gln Tyr Ile Glu Met Trp Ala Asn Val Pro Val  
 305 310 315 320

Glu Val His Val Ala Ser Glu Phe Ser Tyr Asn Met Pro Leu Leu Ser  
 325 330 335

Lys Lys Pro Leu Phe Ile Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp

340					345					350					
Ser	Arg	Ala	Val	Leu	Val	Gln	Val	Lys	Ala	Leu	Gly	His	Lys	Ala	Leu
		355					360					365			
Thr	Ile	Thr	Asn	Val	Pro	Gly	Ser	Thr	Leu	Ser	Arg	Glu	Ala	Asp	Tyr
	370					375					380				
Thr	Leu	Leu	Leu	His	Ala	Gly	Pro	Glu	Ile	Ala	Val	Ala	Ser	Thr	Lys
385					390					395					400
Ala	Tyr	Thr	Ala	Gln	Ile	Ala	Val	Leu	Ala	Val	Leu	Ala	Ser	Val	Ala
				405					410					415	
Ala	Asp	Lys	Asn	Gly	Ile	Asn	Ile	Gly	Phe	Asp	Leu	Val	Lys	Glu	Leu
			420					425					430		
Gly	Ile	Ala	Ala	Asn	Ala	Met	Glu	Ala	Leu	Cys	Asp	Gln	Lys	Asp	Glu
	435						440					445			
Met	Glu	Met	Ile	Ala	Arg	Glu	Tyr	Leu	Thr	Val	Ser	Arg	Asn	Ala	Phe
	450					455					460				
Phe	Ile	Gly	Arg	Gly	Leu	Asp	Tyr	Phe	Val	Cys	Val	Glu	Gly	Ala	Leu
465					470					475					480
Lys	Leu	Lys	Glu	Ile	Ser	Tyr	Ile	Gln	Ala	Glu	Gly	Phe	Ala	Gly	Gly
				485					490					495	
Glu	Leu	Lys	His	Gly	Thr	Ile	Ala	Leu	Ile	Glu	Gln	Gly	Thr	Pro	Val
			500					505					510		
Phe	Ala	Leu	Ala	Thr	Gln	Glu	His	Val	Asn	Leu	Ser	Ile	Arg	Gly	Asn
		515					520					525			
Val	Lys	Glu	Val	Ala	Ala	Arg	Gly	Ala	Asn	Thr	Cys	Ile	Ile	Ser	Leu
	530					535					540				
Lys	Gly	Leu	Asp	Asp	Ala	Asp	Asp	Arg	Phe	Val	Leu	Pro	Glu	Val	Asn
545					550					555					560
Pro	Ala	Leu	Ala	Pro	Leu	Val	Ser	Val	Val	Pro	Leu	Gln	Leu	Ile	Ala
				565					570					575	
Tyr	Tyr	Ala	Ala	Leu	His	Arg	Gly	Cys	Asp	Val	Asp	Lys	Pro	Arg	Asn
		580						585					590		

Leu Ala Lys Ser Val Thr Val Glu  
595 600

<210> 28  
<211> 2154  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)..(2154)

<400> 28  
atg tgt ggt atc ttt ggt tac tgc aat tat cta gtg gaa aga tcc aga 48  
Met Cys Gly Ile Phe Gly Tyr Cys Asn Tyr Leu Val Glu Arg Ser Arg  
1 5 10 15  
gga gaa att atc gac acc tta gtg gat ggt tta caa aga tta gaa tat 96  
Gly Glu Ile Ile Asp Thr Leu Val Asp Gly Leu Gln Arg Leu Glu Tyr  
20 25 30  
aga ggc tat gat tcc acc ggt att gct atc gat ggt gac gaa gct gat 144  
Arg Gly Tyr Asp Ser Thr Gly Ile Ala Ile Asp Gly Asp Glu Ala Asp  
35 40 45  
tct act ttc atc tat aag caa atc ggt aaa gtg agt gct ttg aaa gag 192  
Ser Thr Phe Ile Tyr Lys Gln Ile Gly Lys Val Ser Ala Leu Lys Glu  
50 55 60  
gag att act aag caa aat ccg aac aga gac gtt act ttt gtc tct cat 240  
Glu Ile Thr Lys Gln Asn Pro Asn Arg Asp Val Thr Phe Val Ser His  
65 70 75 80  
tgt ggt att gcg cat act aga tgg gct act cac ggt cga cca gaa caa 288  
Cys Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Arg Pro Glu Gln  
85 90 95  
gtt aac tgt cac cct caa aga tct gac cca gaa gac caa ttt gtg gtc 336  
Val Asn Cys His Pro Gln Arg Ser Asp Pro Glu Asp Gln Phe Val Val  
100 105 110  
gtt cat aat ggt atc atc aca aat ttt aga gaa ctg aag act ctt tta 384  
Val His Asn Gly Ile Ile Thr Asn Phe Arg Glu Leu Lys Thr Leu Leu  
115 120 125  
att aac aaa ggt tat aaa ttc gaa agt gat acc gat acc gag tgt att 432  
Ile Asn Lys Gly Tyr Lys Phe Glu Ser Asp Thr Asp Thr Glu Cys Ile  
130 135 140  
gct aaa cta tat ttg cat tta tac aat aca aat tta caa aat ggg cat 480  
Ala Lys Leu Tyr Leu His Leu Tyr Asn Thr Asn Leu Gln Asn Gly His  
145 150 155 160  
gac tta gat ttc cac gaa tta acc aag cta gtt ctt tta gaa cta gaa 528  
Asp Leu Asp Phe His Glu Leu Thr Lys Leu Val Leu Leu Glu Leu Glu  
165 170 175  
ggt tca tac ggg tta tta tgt aaa tct tgt cac tat cct aat gag gtt 576  
Gly Ser Tyr Gly Leu Leu Cys Lys Ser Cys His Tyr Pro Asn Glu Val  
180 185 190

atc gcc act aga aaa ggg tcc cct tta ctg att ggt gtc aaa tct gaa Ile Ala Thr Arg Lys Gly Ser Pro Leu Leu Ile Gly Val Lys Ser Glu 195 200 205	624
aaa aaa cta aaa gtc gac ttc gtg gat gtg gaa ttt ccc gaa gaa aac Lys Lys Leu Lys Val Asp Phe Val Asp Val Glu Phe Pro Glu Glu Asn 210 215 220	672
gct ggt caa ccg gaa att cca ttg aaa tct aac aac aaa tca ttt ggc Ala Gly Gln Pro Glu Ile Pro Leu Lys Ser Asn Asn Lys Ser Phe Gly 225 230 235 240	720
ttg ggc cca aag aaa gct cgt gaa ttt gaa gct ggt tcc caa aat gcc Leu Gly Pro Lys Lys Ala Arg Glu Phe Glu Ala Gly Ser Gln Asn Ala 245 250 255	768
aat tta cta cca att gcc gcc aat gaa ttt aac ttg aga cat tct caa Asn Leu Leu Pro Ile Ala Ala Asn Glu Phe Asn Leu Arg His Ser Gln 260 265 270	816
tcc agg gct ttc cta tca gaa gat gga tct cca aca ccg gtg gaa ttt Ser Arg Ala Phe Leu Ser Glu Asp Gly Ser Pro Thr Pro Val Glu Phe 275 280 285	864
ttt gtt tct tcg gat gcg gca tct gtt gtt aaa cat acc aag aag gtg Phe Val Ser Ser Asp Ala Ala Ser Val Val Lys His Thr Lys Lys Val 290 295 300	912
cta ttt tta gaa gat gac gat ttg gct cat att tac gat ggt gag tta Leu Phe Leu Glu Asp Asp Asp Leu Ala His Ile Tyr Asp Gly Glu Leu 305 310 315 320	960
cat att cat aga tct aga aga gaa gta ggc gca tca atg aca agg tcc His Ile His Arg Ser Arg Arg Glu Val Gly Ala Ser Met Thr Arg Ser 325 330 335	1008
att caa act tta gag atg gag tta gct cag atc atg aag ggc cct tac Ile Gln Thr Leu Glu Met Glu Leu Ala Gln Ile Met Lys Gly Pro Tyr 340 345 350	1056
gac cat ttt atg caa aag gaa atc tat gag caa cca gaa tct act ttc Asp His Phe Met Gln Lys Glu Ile Tyr Glu Gln Pro Glu Ser Thr Phe 355 360 365	1104
aat act atg aga ggt aga atc gac tat gaa aat aat aaa gtg ata ttg Asn Thr Met Arg Gly Arg Ile Asp Tyr Glu Asn Asn Lys Val Ile Leu 370 375 380	1152
ggt ggt tta aag gca tgg tta cca gtt gtc aga aga gca cgg aga ctg Gly Gly Leu Lys Ala Trp Leu Pro Val Val Arg Arg Ala Arg Arg Leu 385 390 395 400	1200
atc atg atc gca tgc ggt act tct tat cat tca tgt ttg gct act cgt Ile Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg 405 410 415	1248
gct atc ttc gaa gaa tta tca gat atc cca gtt agt gtg gaa tta gcg Ala Ile Phe Glu Glu Leu Ser Asp Ile Pro Val Ser Val Glu Leu Ala 420 425 430	1296
tct gac ttt ctg gac aga aaa tgc cct gtc ttc aga gac gat gta tgc Ser Asp Phe Leu Asp Arg Lys Cys Pro Val Phe Arg Asp Asp Val Cys	1344

435	440	445	
gtg ttt gtt tca caa agt ggt gaa act gcg gat acc atg ctg gct cta Val Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Thr Met Leu Ala Leu 450 455 460			1392
aat tat tgt tta gaa aga gga gcc tta act gtc gga att gtt aac agt Asn Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser 465 470 475 480			1440
gtt ggt tct tct atc tct cgt gtc acc cac tgt ggt gtt cat att aac Val Gly Ser Ser Ile Ser Arg Val Thr His Cys Gly Val His Ile Asn 485 490 495			1488
gct ggt cct gaa att ggt gtt gcc tct aca aaa gct tat act tcc cag Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln 500 505 510			1536
tat att gcc tta gtg atg ttt gct cta tcg ctg tca gat gac cgt gta Tyr Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asp Asp Arg Val 515 520 525			1584
tcg aaa ata gac aga aga att gaa atc att caa ggc ttg aag tta atc Ser Lys Ile Asp Arg Arg Ile Glu Ile Ile Gln Gly Leu Lys Leu Ile 530 535 540			1632
ccg ggc caa att aag cag gta tta aag ctg gaa cca aga ata aaa aag Pro Gly Gln Ile Lys Gln Val Leu Lys Leu Glu Pro Arg Ile Lys Lys 545 550 555 560			1680
ctc tgt gcg act gaa tta aag gat caa aaa tct cta ttg tta ttg ggt Leu Cys Ala Thr Glu Leu Lys Asp Gln Lys Ser Leu Leu Leu Gly 565 570 575			1728
aga ggt tac caa ttt gct gct gct ctg gaa ggt gct ttg aag atc aaa Arg Gly Tyr Gln Phe Ala Ala Leu Glu Gly Ala Leu Lys Ile Lys 580 585 590			1776
gaa att tct tat atg cat tct gaa ggt gtt ttg gca ggt gag ttg aag Glu Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys 595 600 605			1824
cac ggt gtc ttg gcc ttg gtg gac gaa aac ttg cca atc att gct ttt His Gly Val Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Ala Phe 610 615 620			1872
ggt acc aga gac tct cta ttc cct aaa gta gtt tcc tct att gag caa Gly Thr Arg Asp Ser Leu Phe Pro Lys Val Val Ser Ser Ile Glu Gln 625 630 635 640			1920
gtt act gca aga aag ggc cat cca att att att tgt aac gaa aat gat Val Thr Ala Arg Lys Gly His Pro Ile Ile Ile Cys Asn Glu Asn Asp 645 650 655			1968
gaa gtg tgg gcg caa aaa tct aaa tca atc gac ctg caa acc tta gaa Glu Val Trp Ala Gln Lys Ser Lys Ser Ile Asp Leu Gln Thr Leu Glu 660 665 670			2016
gtt cca caa act gtt gat tgt tta caa ggt cta att aat att att cca Val Pro Gln Thr Val Asp Cys Leu Gln Gly Leu Ile Asn Ile Ile Pro 675 680 685			2064

tta caa cta atg tca tat tgg ttg gct gtt aat aaa ggg att gat gtt 2112  
 Leu Gln Leu Met Ser Tyr Trp Leu Ala Val Asn Lys Gly Ile Asp Val  
 690 695 700

gat ttt cca aga aac ttg gct aaa tct gtt acc gtc gaa taa 2154  
 Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
 705 710 715

<210> 29  
 <211> 717  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 29

Met Cys Gly Ile Phe Gly Tyr Cys Asn Tyr Leu Val Glu Arg Ser Arg  
 1 5 10 15

Gly Glu Ile Ile Asp Thr Leu Val Asp Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30

Arg Gly Tyr Asp Ser Thr Gly Ile Ala Ile Asp Gly Asp Glu Ala Asp  
 35 40 45

Ser Thr Phe Ile Tyr Lys Gln Ile Gly Lys Val Ser Ala Leu Lys Glu  
 50 55 60

Glu Ile Thr Lys Gln Asn Pro Asn Arg Asp Val Thr Phe Val Ser His  
 65 70 75 80

Cys Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Arg Pro Glu Gln  
 85 90 95

Val Asn Cys His Pro Gln Arg Ser Asp Pro Glu Asp Gln Phe Val Val  
 100 105 110

Val His Asn Gly Ile Ile Thr Asn Phe Arg Glu Leu Lys Thr Leu Leu  
 115 120 125

Ile Asn Lys Gly Tyr Lys Phe Glu Ser Asp Thr Asp Thr Glu Cys Ile  
 130 135 140

Ala Lys Leu Tyr Leu His Leu Tyr Asn Thr Asn Leu Gln Asn Gly His  
 145 150 155 160

Asp Leu Asp Phe His Glu Leu Thr Lys Leu Val Leu Leu Glu Leu Glu  
 165 170 175

Gly Ser Tyr Gly Leu Leu Cys Lys Ser Cys His Tyr Pro Asn Glu Val  
 180 185 190



Ile Ala Thr Arg Lys Gly Ser Pro Leu Leu Ile Gly Val Lys Ser Glu  
 195 200 205

Lys Lys Leu Lys Val Asp Phe Val Asp Val Glu Phe Pro Glu Glu Asn  
 210 215 220

Ala Gly Gln Pro Glu Ile Pro Leu Lys Ser Asn Asn Lys Ser Phe Gly  
 225 230 235 240

Leu Gly Pro Lys Lys Ala Arg Glu Phe Glu Ala Gly Ser Gln Asn Ala  
 245 250 255

Asn Leu Leu Pro Ile Ala Ala Asn Glu Phe Asn Leu Arg His Ser Gln  
 260 265 270

Ser Arg Ala Phe Leu Ser Glu Asp Gly Ser Pro Thr Pro Val Glu Phe  
 275 280 285

Phe Val Ser Ser Asp Ala Ala Ser Val Val Lys His Thr Lys Lys Val  
 290 295 300

Leu Phe Leu Glu Asp Asp Asp Leu Ala His Ile Tyr Asp Gly Glu Leu  
 305 310 315 320

His Ile His Arg Ser Arg Arg Glu Val Gly Ala Ser Met Thr Arg Ser  
 325 330 335

Ile Gln Thr Leu Glu Met Glu Leu Ala Gln Ile Met Lys Gly Pro Tyr  
 340 345 350

Asp His Phe Met Gln Lys Glu Ile Tyr Glu Gln Pro Glu Ser Thr Phe  
 355 360 365

Asn Thr Met Arg Gly Arg Ile Asp Tyr Glu Asn Asn Lys Val Ile Leu  
 370 375 380

Gly Gly Leu Lys Ala Trp Leu Pro Val Val Arg Arg Ala Arg Arg Leu  
 385 390 395 400

Ile Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg  
 405 410 415

Ala Ile Phe Glu Glu Leu Ser Asp Ile Pro Val Ser Val Glu Leu Ala  
 420 425 430

Ser Asp Phe Leu Asp Arg Lys Cys Pro Val Phe Arg Asp Asp Val Cys

435	440	445
Val Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Thr Met Leu Ala Leu 450 455 460		
Asn Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser 465 470 475 480		
Val Gly Ser Ser Ile Ser Arg Val Thr His Cys Gly Val His Ile Asn 485 490 495		
Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln 500 505 510		
Tyr Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asp Asp Arg Val 515 520 525		
Ser Lys Ile Asp Arg Arg Ile Glu Ile Ile Gln Gly Leu Lys Leu Ile 530 535 540		
Pro Gly Gln Ile Lys Gln Val Leu Lys Leu Glu Pro Arg Ile Lys Lys 545 550 555 560		
Leu Cys Ala Thr Glu Leu Lys Asp Gln Lys Ser Leu Leu Leu Leu Gly 565 570 575		
Arg Gly Tyr Gln Phe Ala Ala Ala Leu Glu Gly Ala Leu Lys Ile Lys 580 585 590		
Glu Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys 595 600 605		
His Gly Val Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Ala Phe 610 615 620		
Gly Thr Arg Asp Ser Leu Phe Pro Lys Val Val Ser Ser Ile Glu Gln 625 630 635 640		
Val Thr Ala Arg Lys Gly His Pro Ile Ile Ile Cys Asn Glu Asn Asp 645 650 655		
Glu Val Trp Ala Gln Lys Ser Lys Ser Ile Asp Leu Gln Thr Leu Glu 660 665 670		
Val Pro Gln Thr Val Asp Cys Leu Gln Gly Leu Ile Asn Ile Ile Pro 675 680 685		

Leu Gln Leu Met Ser Tyr Trp Leu Ala Val Asn Lys Gly Ile Asp Val  
690 695 700

Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
705 710 715

<210> 30  
<211> 2142  
<212> DNA  
<213> Candida albicans

<220>  
<221> CDS  
<222> (1)..(2142)

<400> 30  
atg tgt ggt att ttt ggt tac gtc aat ttc ttg gtc gac aag agt aga 48  
Met Cys Gly Ile Phe Gly Tyr Val Asn Phe Leu Val Asp Lys Ser Arg  
1 5 10 15  
ggt gaa atc att gat aat tta att gaa ggt ttg caa cga tta gaa tat 96  
Gly Glu Ile Ile Asp Asn Leu Ile Glu Gly Leu Gln Arg Leu Glu Tyr  
20 25 30  
aga ggt tat gat tca gca ggc att gct gtt gat ggg aaa tta act aaa 144  
Arg Gly Tyr Asp Ser Ala Gly Ile Ala Val Asp Gly Lys Leu Thr Lys  
35 40 45  
gat cct tct aat ggt gat gaa gaa tat atg gat tct att att gtt aaa 192  
Asp Pro Ser Asn Gly Asp Glu Glu Tyr Met Asp Ser Ile Ile Val Lys  
50 55 60  
act act ggt aaa gtt aaa gtt ttg aaa caa aaa atc att gat gat caa 240  
Thr Thr Gly Lys Val Lys Val Leu Lys Gln Lys Ile Ile Asp Asp Gln  
65 70 75 80  
atc gat aga tcg gcc att ttt gat aat cat gtt ggt att gct cat act 288  
Ile Asp Arg Ser Ala Ile Phe Asp Asn His Val Gly Ile Ala His Thr  
85 90 95  
aga tgg gct aca cat ggt caa cca aaa act gaa aat tgt cat cct cat 336  
Arg Trp Ala Thr His Gly Gln Pro Lys Thr Glu Asn Cys His Pro His  
100 105 110  
aaa tca gat cca aag ggg gaa ttc att gtt gtt cat aat ggt att att 384  
Lys Ser Asp Pro Lys Gly Glu Phe Ile Val Val His Asn Gly Ile Ile  
115 120 125  
act aat tat gct gct tta aga aaa tat ctt tta tca aaa gga cat gtt 432  
Thr Asn Tyr Ala Ala Leu Arg Lys Tyr Leu Leu Ser Lys Gly His Val  
130 135 140  
ttt gaa agt gaa act gat act gaa tgt att gct aaa tta ttt aaa cat 480  
Phe Glu Ser Glu Thr Asp Thr Glu Cys Ile Ala Lys Leu Phe Lys His  
145 150 155 160  
ttt tat gat ttg aat gtt aaa gct ggt gtt ttc cct gat ctt aat gaa 528  
Phe Tyr Asp Leu Asn Val Lys Ala Gly Val Phe Pro Asp Leu Asn Glu  
165 170 175

ttg act aaa caa gtt ttg cat gaa tta gaa ggt tct tat ggg tta tta Leu Thr Lys Gln Val Leu His Glu Leu Glu Gly Ser Tyr Gly Leu Leu 180 185 190	576
gtt aaa tct tat cat tat cct gga gaa gtt tgt ggt act aga aaa ggt Val Lys Ser Tyr His Tyr Pro Gly Glu Val Cys Gly Thr Arg Lys Gly 195 200 205	624
tct cca tta ttg gtt ggt gtt aaa act gat aag aaa tta aaa gtt gat Ser Pro Leu Leu Val Gly Val Lys Thr Asp Lys Lys Leu Lys Val Asp 210 215 220	672
ttt gtt gac gtt gaa ttt gaa gct caa cag caa cat cga cca caa caa Phe Val Asp Val Glu Phe Glu Ala Gln Gln His Arg Pro Gln Gln 225 230 235 240	720
cca caa atc aat cat aat ggt gcc act tca gct gct gaa ttg ggc ttt Pro Gln Ile Asn His Asn Gly Ala Thr Ser Ala Ala Glu Leu Gly Phe 245 250 255	768
atc cca gtg gct cca ggt gaa caa aat tta aga act tct caa tca aga Ile Pro Val Ala Pro Gly Glu Gln Asn Leu Arg Thr Ser Gln Ser Arg 260 265 270	816
gct ttc ctt tct gaa gat gat tta cct atg cca gtt gaa ttc ttt tta Ala Phe Leu Ser Glu Asp Asp Leu Pro Met Pro Val Glu Phe Phe Leu 275 280 285	864
tct tct gat cct gca tca gtg gtt caa cac acc aaa aaa gtt tta ttt Ser Ser Asp Pro Ala Ser Val Gln His Thr Lys Lys Val Leu Phe 290 295 300	912
tta gaa gat gat gat att gct cat atc tat gat ggg gaa tta cgt att Leu Glu Asp Asp Asp Ile Ala His Ile Tyr Asp Gly Glu Leu Arg Ile 305 310 315 320	960
cat aga gct tcg act aaa tct gct ggg gaa tct act gtt aga cca att His Arg Ala Ser Thr Lys Ser Ala Gly Glu Ser Thr Val Arg Pro Ile 325 330 335	1008
caa act tta gaa atg gaa ttg aat gaa att atg aaa ggc ccc tat aaa Gln Thr Leu Glu Met Glu Leu Asn Glu Ile Met Lys Gly Pro Tyr Lys 340 345 350	1056
cat ttt atg caa aaa gaa att ttc gaa caa cca gat tct gct ttt aat His Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Asp Ser Ala Phe Asn 355 360 365	1104
act atg aga ggt aga att gat ttt gaa aat tgt gtt gtt acc ctt ggt Thr Met Arg Gly Arg Ile Asp Phe Glu Asn Cys Val Val Thr Leu Gly 370 375 380	1152
gga tta aaa tca tgg tta tct aca att aga aga tgt aga aga atc att Gly Leu Lys Ser Trp Leu Ser Thr Ile Arg Arg Cys Arg Arg Ile Ile 385 390 395 400	1200
atg att gct tgt ggt act tca tat cat tca tgt tta gcc acg aga tca Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg Ser 405 410 415	1248
att ttt gaa gaa ttg aca gaa atc ccc gtt tcg gtt gaa tta gct tct Ile Phe Glu Glu Leu Thr Glu Ile Pro Val Ser Val Glu Leu Ala Ser	1296

420										425					430					
gat	ttc	ttg	gat	aga	aga	tct	cca	ggt	ttc	aga	gat	gat	act	tgt	gta	1344				
Asp	Phe	Leu	Asp	Arg	Arg	Ser	Pro	Val	Phe	Arg	Asp	Asp	Thr	Cys	Val					
		435					440					445								
ttt	ggt	tct	caa	tcg	ggt	gaa	act	gcc	gac	tcc	att	ttg	gct	tta	caa	1392				
Phe	Val	Ser	Gln	Ser	Gly	Glu	Thr	Ala	Asp	Ser	Ile	Leu	Ala	Leu	Gln					
	450					455					460									
tat	tgt	ttg	gaa	aga	gga	gct	tta	act	ggt	ggg	atc	ggt	aac	tct	ggt	1440				
Tyr	Cys	Leu	Glu	Arg	Gly	Ala	Leu	Thr	Val	Gly	Ile	Val	Asn	Ser	Val					
465					470					475					480					
ggt	tct	tca	atg	tct	aga	caa	acc	cat	tgt	ggg	ggt	cat	att	aat	gct	1488				
Gly	Ser	Ser	Met	Ser	Arg	Gln	Thr	His	Cys	Gly	Val	His	Ile	Asn	Ala					
				485					490					495						
ggg	cca	gaa	att	ggt	ggt	gcc	tca	act	aaa	gct	tac	aca	tct	caa	tat	1536				
Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Tyr					
			500					505					510							
att	gcc	ttg	gtg	atg	ttt	gcc	ctt	tct	tta	tct	aat	gat	tct	att	tcc	1584				
Ile	Ala	Leu	Val	Met	Phe	Ala	Leu	Ser	Leu	Ser	Asn	Asp	Ser	Ile	Ser					
		515					520					525								
aga	aag	gga	aga	cat	gaa	gaa	att	att	aaa	ggt	tta	caa	aaa	atc	cct	1632				
Arg	Lys	Gly	Arg	His	Glu	Glu	Ile	Ile	Lys	Gly	Leu	Gln	Lys	Ile	Pro					
	530					535					540									
gaa	caa	att	aaa	caa	ggt	ttg	aaa	tta	gaa	aac	aag	atc	aaa	gat	tta	1680				
Glu	Gln	Ile	Lys	Gln	Val	Leu	Lys	Leu	Glu	Asn	Lys	Ile	Lys	Asp	Leu					
545					550					555					560					
tgt	aat	agt	tca	ttg	aat	gat	caa	aaa	tct	tta	tta	tta	tta	ggt	aga	1728				
Cys	Asn	Ser	Ser	Leu	Asn	Asp	Gln	Lys	Ser	Leu	Leu	Leu	Leu	Gly	Arg					
				565				570						575						
ggt	tat	caa	ttt	gct	act	gct	tta	gaa	ggg	gct	tta	aaa	att	aaa	gaa	1776				
Gly	Tyr	Gln	Phe	Ala	Thr	Ala	Leu	Glu	Gly	Ala	Leu	Lys	Ile	Lys	Glu					
			580				585						590							
att	tct	tat	atg	cat	tct	gaa	ggg	gta	tta	gct	ggt	gaa	tta	aaa	cat	1824				
Ile	Ser	Tyr	Met	His	Ser	Glu	Gly	Val	Leu	Ala	Gly	Glu	Leu	Lys	His					
		595					600					605								
ggt	ata	tta	gca	tta	gtc	gat	gaa	gat	tta	cca	att	att	gcc	ttt	gcc	1872				
Gly	Ile	Leu	Ala	Leu	Val	Asp	Glu	Asp	Leu	Pro	Ile	Ile	Ala	Phe	Ala					
	610					615					620									
act	aga	gat	tca	tta	ttt	cct	aaa	ggt	atg	tcc	gct	att	gaa	caa	gtc	1920				
Thr	Arg	Asp	Ser	Leu	Phe	Pro	Lys	Val	Met	Ser	Ala	Ile	Glu	Gln	Val					
625					630					635					640					
act	gct	aga	gat	ggt	aga	cca	att	ggt	att	tgt	aat	gaa	ggt	gat	gct	1968				
Thr	Ala	Arg	Asp	Gly	Arg	Pro	Ile	Val	Ile	Cys	Asn	Glu	Gly	Asp	Ala					
				645				650						655						
att	att	tct	aat	gat	aaa	ggt	cat	act	act	tta	gaa	ggt	cca	gaa	acc	2016				
Ile	Ile	Ser	Asn	Asp	Lys	Val	His	Thr	Thr	Leu	Glu	Val	Pro	Glu	Thr					
			660					665					670							

gtt gat tgt tta caa ggg tta tta aat gtt att cca tta caa ttg att 2064  
 Val Asp Cys Leu Gln Gly Leu Leu Asn Val Ile Pro Leu Gln Leu Ile  
 675 680 685

agt tat tgg ttg gct gtg aat aga ggt att gat gtt gat ttc cct cgt 2112  
 Ser Tyr Trp Leu Ala Val Asn Arg Gly Ile Asp Val Asp Phe Pro Arg  
 690 695 700

aac ttg gct aaa tca gtt act gtt gag taa 2142  
 Asn Leu Ala Lys Ser Val Thr Val Glu  
 705 710

<210> 31  
 <211> 713  
 <212> PRT  
 <213> Candida albicans

<400> 31

Met Cys Gly Ile Phe Gly Tyr Val Asn Phe Leu Val Asp Lys Ser Arg  
 1 5 10 15

Gly Glu Ile Ile Asp Asn Leu Ile Glu Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30

Arg Gly Tyr Asp Ser Ala Gly Ile Ala Val Asp Gly Lys Leu Thr Lys  
 35 40 45

Asp Pro Ser Asn Gly Asp Glu Glu Tyr Met Asp Ser Ile Ile Val Lys  
 50 55 60

Thr Thr Gly Lys Val Lys Val Leu Lys Gln Lys Ile Ile Asp Asp Gln  
 65 70 75 80

Ile Asp Arg Ser Ala Ile Phe Asp Asn His Val Gly Ile Ala His Thr  
 85 90 95

Arg Trp Ala Thr His Gly Gln Pro Lys Thr Glu Asn Cys His Pro His  
 100 105 110

Lys Ser Asp Pro Lys Gly Glu Phe Ile Val Val His Asn Gly Ile Ile  
 115 120 125

Thr Asn Tyr Ala Ala Leu Arg Lys Tyr Leu Leu Ser Lys Gly His Val  
 130 135 140

Phe Glu Ser Glu Thr Asp Thr Glu Cys Ile Ala Lys Leu Phe Lys His  
 145 150 155 160

Phe Tyr Asp Leu Asn Val Lys Ala Gly Val Phe Pro Asp Leu Asn Glu  
 165 170 175

Leu Thr Lys Gln Val Leu His Glu Leu Glu Gly Ser Tyr Gly Leu Leu  
 180 185 190

Val Lys Ser Tyr His Tyr Pro Gly Glu Val Cys Gly Thr Arg Lys Gly  
 195 200 205

Ser Pro Leu Leu Val Gly Val Lys Thr Asp Lys Lys Leu Lys Val Asp  
 210 215 220

Phe Val Asp Val Glu Phe Glu Ala Gln Gln Gln His Arg Pro Gln Gln  
 225 230 235 240

Pro Gln Ile Asn His Asn Gly Ala Thr Ser Ala Ala Glu Leu Gly Phe  
 245 250 255

Ile Pro Val Ala Pro Gly Glu Gln Asn Leu Arg Thr Ser Gln Ser Arg  
 260 265 270

Ala Phe Leu Ser Glu Asp Asp Leu Pro Met Pro Val Glu Phe Phe Leu  
 275 280 285

Ser Ser Asp Pro Ala Ser Val Val Gln His Thr Lys Lys Val Leu Phe  
 290 295 300

Leu Glu Asp Asp Asp Ile Ala His Ile Tyr Asp Gly Glu Leu Arg Ile  
 305 310 315 320

His Arg Ala Ser Thr Lys Ser Ala Gly Glu Ser Thr Val Arg Pro Ile  
 325 330 335

Gln Thr Leu Glu Met Glu Leu Asn Glu Ile Met Lys Gly Pro Tyr Lys  
 340 345 350

His Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Asp Ser Ala Phe Asn  
 355 360 365

Thr Met Arg Gly Arg Ile Asp Phe Glu Asn Cys Val Val Thr Leu Gly  
 370 375 380

Gly Leu Lys Ser Trp Leu Ser Thr Ile Arg Arg Cys Arg Arg Ile Ile  
 385 390 395 400

Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg Ser  
 405 410 415

Ile Phe Glu Glu Leu Thr Glu Ile Pro Val Ser Val Glu Leu Ala Ser

			420					425					430				
Asp	Phe	Leu	Asp	Arg	Arg	Ser	Pro	Val	Phe	Arg	Asp	Asp	Thr	Cys	Val		
		435					440					445					
Phe	Val	Ser	Gln	Ser	Gly	Glu	Thr	Ala	Asp	Ser	Ile	Leu	Ala	Leu	Gln		
		450					455					460					
Tyr	Cys	Leu	Glu	Arg	Gly	Ala	Leu	Thr	Val	Gly	Ile	Val	Asn	Ser	Val		
465					470					475							
Gly	Ser	Ser	Met	Ser	Arg	Gln	Thr	His	Cys	Gly	Val	His	Ile	Asn	Ala		
				485					490					495			
Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Tyr		
				500					505					510			
Ile	Ala	Leu	Val	Met	Phe	Ala	Leu	Ser	Leu	Ser	Asn	Asp	Ser	Ile	Ser		
		515					520					525					
Arg	Lys	Gly	Arg	His	Glu	Glu	Ile	Ile	Lys	Gly	Leu	Gln	Lys	Ile	Pro		
		530					535					540					
Glu	Gln	Ile	Lys	Gln	Val	Leu	Lys	Leu	Glu	Asn	Lys	Ile	Lys	Asp	Leu		
545					550					555							
Cys	Asn	Ser	Ser	Leu	Asn	Asp	Gln	Lys	Ser	Leu	Leu	Leu	Leu	Gly	Arg		
				565					570					575			
Gly	Tyr	Gln	Phe	Ala	Thr	Ala	Leu	Glu	Gly	Ala	Leu	Lys	Ile	Lys	Glu		
				580					585					590			
Ile	Ser	Tyr	Met	His	Ser	Glu	Gly	Val	Leu	Ala	Gly	Glu	Leu	Lys	His		
		595					600					605					
Gly	Ile	Leu	Ala	Leu	Val	Asp	Glu	Asp	Leu	Pro	Ile	Ile	Ala	Phe	Ala		
		610					615					620					
Thr	Arg	Asp	Ser	Leu	Phe	Pro	Lys	Val	Met	Ser	Ala	Ile	Glu	Gln	Val		
625					630					635							
Thr	Ala	Arg	Asp	Gly	Arg	Pro	Ile	Val	Ile	Cys	Asn	Glu	Gly	Asp	Ala		
				645					650					655			
Ile	Ile	Ser	Asn	Asp	Lys	Val	His	Thr	Thr	Leu	Glu	Val	Pro	Glu	Thr		
				660					665					670			



Val Asp Cys Leu Gln Gly Leu Leu Asn Val Ile Pro Leu Gln Leu Ile  
675 680 685

Ser Tyr Trp Leu Ala Val Asn Arg Gly Ile Asp Val Asp Phe Pro Arg  
690 695 700

Asn Leu Ala Lys Ser Val Thr Val Glu  
705 710

<210> 32  
<211> 480  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)..(480)

<400> 32  
atg agc tta ccc gat gga ttt tat ata agg cga atg gaa gag ggg gat 48  
Met Ser Leu Pro Asp Gly Phe Tyr Ile Arg Arg Met Glu Glu Gly Asp  
1 5 10 15  
ttg gaa cag gtc act gag acg cta aag gtt ttg acc acc gtg ggc act 96  
Leu Glu Gln Val Thr Glu Thr Leu Lys Val Leu Thr Thr Val Gly Thr  
20 25 30  
att acc ccc gaa tcc ttc agc aaa ctc ata aaa tac tgg aat gaa gcc 144  
Ile Thr Pro Glu Ser Phe Ser Lys Leu Ile Lys Tyr Trp Asn Glu Ala  
35 40 45  
aca gta tgg aat gat aac gaa gat aaa aaa ata atg caa tat aac ccc 192  
Thr Val Trp Asn Asp Asn Glu Asp Lys Lys Ile Met Gln Tyr Asn Pro  
50 55 60  
atg gtg att gtg gac aag cgc acc gag acg gtt gcc gct acg ggg aat 240  
Met Val Ile Val Asp Lys Arg Thr Glu Thr Val Ala Ala Thr Gly Asn  
65 70 75 80  
atc atc atc gaa aga aag atc att cat gaa ctg ggg cta tgt ggc cac 288  
Ile Ile Ile Glu Arg Lys Ile Ile His Glu Leu Gly Leu Cys Gly His  
85 90 95  
atc gag gac att gca gta aac tcc aag tat cag ggc caa ggt ttg ggc 336  
Ile Glu Asp Ile Ala Val Asn Ser Lys Tyr Gln Gly Gln Gly Leu Gly  
100 105 110  
aag ctc ttg att gat caa ttg gta act atc ggc ttt gac tac ggt tgt 384  
Lys Leu Leu Ile Asp Gln Leu Val Thr Ile Gly Phe Asp Tyr Gly Cys  
115 120 125  
tat aag att att tta gat tgc gat gag aaa aat gtc aaa ttc tat gaa 432  
Tyr Lys Ile Ile Leu Asp Cys Asp Glu Lys Asn Val Lys Phe Tyr Glu  
130 135 140  
aaa tgt ggg ttt agc aac gca ggc gtg gaa atg caa att aga aaa tag 480  
Lys Cys Gly Phe Ser Asn Ala Gly Val Glu Met Gln Ile Arg Lys  
145 150 155

<210> 33  
 <211> 159  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 33

Met Ser Leu Pro Asp Gly Phe Tyr Ile Arg Arg Met Glu Glu Gly Asp  
 1 5 10 15

Leu Glu Gln Val Thr Glu Thr Leu Lys Val Leu Thr Thr Val Gly Thr  
 20 25 30

Ile Thr Pro Glu Ser Phe Ser Lys Leu Ile Lys Tyr Trp Asn Glu Ala  
 35 40 45

Thr Val Trp Asn Asp Asn Glu Asp Lys Lys Ile Met Gln Tyr Asn Pro  
 50 55 60

Met Val Ile Val Asp Lys Arg Thr Glu Thr Val Ala Ala Thr Gly Asn  
 65 70 75 80

Ile Ile Ile Glu Arg Lys Ile Ile His Glu Leu Gly Leu Cys Gly His  
 85 90 95

Ile Glu Asp Ile Ala Val Asn Ser Lys Tyr Gln Gly Gln Gly Leu Gly  
 100 105 110

Lys Leu Leu Ile Asp Gln Leu Val Thr Ile Gly Phe Asp Tyr Gly Cys  
 115 120 125

Tyr Lys Ile Ile Leu Asp Cys Asp Glu Lys Asn Val Lys Phe Tyr Glu  
 130 135 140

Lys Cys Gly Phe Ser Asn Ala Gly Val Glu Met Gln Ile Arg Lys  
 145 150 155

<210> 34  
 <211> 450  
 <212> DNA  
 <213> *Candida albicans*

<220>  
 <221> CDS  
 <222> (1)..(450)

<400> 34

atg atg tta cca caa ggt tat aca ttc aga aaa cta aaa ctt act gat  
 Met Met Leu Pro Gln Gly Tyr Thr Phe Arg Lys Leu Lys Leu Thr Asp  
 1 5 10 15

48

tat gat aat caa tat tta gaa act tta aaa gtt ttg acg aca gtt ggt Tyr Asp Asn Gln Tyr Leu Glu Thr Leu Lys Val Leu Thr Thr Val Gly 20 25 30	96
gaa att tcc aaa gaa gat ttc act gaa ttg tat aat cat tgg tct tca Glu Ile Ser Lys Glu Asp Phe Thr Glu Leu Tyr Asn His Trp Ser Ser 35 40 45	144
ttg cca tct att tat cat cca tat gta atc acc aat gca tca ggt ata Leu Pro Ser Ile Tyr His Pro Tyr Val Ile Thr Asn Ala Ser Gly Ile 50 55 60	192
gtg gta gcc acg ggg atg tta ttt gtg gag aaa aaa ttg att cat gaa Val Val Ala Thr Gly Met Leu Phe Val Glu Lys Lys Leu Ile His Glu 65 70 75 80	240
tgt ggt aaa gtt ggt cat att gaa gat att tca gtt gct aaa tct gaa Cys Gly Lys Val Gly His Ile Glu Asp Ile Ser Val Ala Lys Ser Glu 85 90 95	288
caa ggt aaa aaa ttg gga tat tat tta gtc act tca tta acc aaa gtt Gln Gly Lys Lys Leu Gly Tyr Tyr Leu Val Thr Ser Leu Thr Lys Val 100 105 110	336
gct caa gag aat gat tgt tac aaa gtc att tta gat tgt tct cct gaa Ala Gln Glu Asn Asp Cys Tyr Lys Val Ile Leu Asp Cys Ser Pro Glu 115 120 125	384
aat gtt ggc ttt tat gaa aaa tgt ggt tat aaa gat ggt ggt gtt gaa Asn Val Gly Phe Tyr Glu Lys Cys Gly Tyr Lys Asp Gly Gly Val Glu 130 135 140	432
atg gta tgt aga ttc tag Met Val Cys Arg Phe 145	450

<210> 35  
 <211> 149  
 <212> PRT  
 <213> Candida albicans

<400> 35

Met Met Leu Pro Gln Gly Tyr Thr Phe Arg Lys Leu Lys Leu Thr Asp 1 5 10 15
Tyr Asp Asn Gln Tyr Leu Glu Thr Leu Lys Val Leu Thr Thr Val Gly 20 25 30
Glu Ile Ser Lys Glu Asp Phe Thr Glu Leu Tyr Asn His Trp Ser Ser 35 40 45
Leu Pro Ser Ile Tyr His Pro Tyr Val Ile Thr Asn Ala Ser Gly Ile 50 55 60
Val Val Ala Thr Gly Met Leu Phe Val Glu Lys Lys Leu Ile His Glu 65 70 75 80

Cys Gly Lys Val Gly His Ile Glu Asp Ile Ser Val Ala Lys Ser Glu  
85 90 95

Gln Gly Lys Lys Leu Gly Tyr Tyr Leu Val Thr Ser Leu Thr Lys Val  
100 105 110

Ala Gln Glu Asn Asp Cys Tyr Lys Val Ile Leu Asp Cys Ser Pro Glu  
115 120 125

Asn Val Gly Phe Tyr Glu Lys Cys Gly Tyr Lys Asp Gly Gly Val Glu  
130 135 140

Met Val Cys Arg Phe  
145

<210> 36  
<211> 906  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)..(906)

<400> 36  
atg aaa att ttc aat aca ata caa tct gtg ctg ttc gca gca ttt ttt 48  
Met Lys Ile Phe Asn Thr Ile Gln Ser Val Leu Phe Ala Ala Phe Phe  
1 5 10 15  
cta aaa cag gga aat tgc ctt gcg tca aat ggg agt acc gca ttg atg 96  
Leu Lys Gln Gly Asn Cys Leu Ala Ser Asn Gly Ser Thr Ala Leu Met  
20 25 30  
ggg gaa gta gat atg caa acg ccc ttt cca gag tgg tta aca gaa ttt 144  
Gly Glu Val Asp Met Gln Thr Pro Phe Pro Glu Trp Leu Thr Glu Phe  
35 40 45  
act aat ctt aca caa tgg cct gga att gac cca cct tat att ccg cta 192  
Thr Asn Leu Thr Gln Trp Pro Gly Ile Asp Pro Pro Tyr Ile Pro Leu  
50 55 60  
gat tac ata aat ctt act gaa gtg cca gaa tta gat agg tac tat cct 240  
Asp Tyr Ile Asn Leu Thr Glu Val Pro Glu Leu Asp Arg Tyr Tyr Pro  
65 70 75 80  
ggc cag tgt ccc aaa att tct aga gag cag tgc tca ttt gac tgc tat 288  
Gly Gln Cys Pro Lys Ile Ser Arg Glu Gln Cys Ser Phe Asp Cys Tyr  
85 90 95  
aac tgc atc gat gtt gat gat gta act tcg tgt ttc aaa ctt tcc caa 336  
Asn Cys Ile Asp Val Asp Asp Val Thr Ser Cys Phe Lys Leu Ser Gln  
100 105 110  
aca ttt gac gac ggt ccg gcc ccg gcg aca gag gca ttg ctc aag aaa 384  
Thr Phe Asp Asp Gly Pro Ala Pro Ala Thr Glu Ala Leu Leu Lys Lys

115	120	125	
ttg aga caa aga acc act ttt ttt gtt ctg ggg ata aac act gtt aat Leu Arg Gln Arg Thr Thr Phe Phe Val Leu Gly Ile Asn Thr Val Asn 130 135 140			432
tat cct gat ata tat gag cat att tta gag agg ggt cat ttg att ggt Tyr Pro Asp Ile Tyr Glu His Ile Leu Glu Arg Gly His Leu Ile Gly 145 150 155 160			480
aca cac acg tgg tca cat gaa ttc ttg cca agt tta tca aac gaa gaa Thr His Thr Trp Ser His Glu Phe Leu Pro Ser Leu Ser Asn Glu Glu 165 170 175			528
att gta gcc caa att gaa tgg tca att tgg gct atg aat gcc aca ggc Ile Val Ala Gln Ile Glu Trp Ser Ile Trp Ala Met Asn Ala Thr Gly 180 185 190			576
aaa cat ttc ccc aag tat ttt agg cct cca tac ggt gca att gat aat Lys His Phe Pro Lys Tyr Phe Arg Pro Pro Tyr Gly Ala Ile Asp Asn 195 200 205			624
agg gtt aga gct ata gta aaa cag ttt ggc cta acg gtt gtc ttg tgg Arg Val Arg Ala Ile Val Lys Gln Phe Gly Leu Thr Val Val Leu Trp 210 215 220			672
gat ctc gat act ttt gat tgg aaa tta atc act aat gat gat ttc aga Asp Leu Asp Thr Phe Asp Trp Lys Leu Ile Thr Asn Asp Asp Phe Arg 225 230 235 240			720
aca gag gaa gaa ata ctt atg gac ata aat act tgg aag gga aaa cgg Thr Glu Glu Glu Ile Leu Met Asp Ile Asn Thr Trp Lys Gly Lys Arg 245 250 255			768
aaa ggt ttg atc tta gag cac gat ggt gca cga aga aca gtt gag gtt Lys Gly Leu Ile Leu Glu His Asp Gly Ala Arg Arg Thr Val Glu Val 260 265 270			816
gct att aaa atc aac gaa ctt att ggt agt gac caa ttg aca att gca Ala Ile Lys Ile Asn Glu Leu Ile Gly Ser Asp Gln Leu Thr Ile Ala 275 280 285			864
gaa tgt att ggt gat aca gac tac atc gaa cgc tac gac tag Glu Cys Ile Gly Asp Thr Asp Tyr Ile Glu Arg Tyr Asp 290 295 300			906

<210> 37  
 <211> 301  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 37

Met	Lys	Ile	Phe	Asn	Thr	Ile	Gln	Ser	Val	Leu	Phe	Ala	Ala	Phe	Phe
1				5					10					15	

Leu	Lys	Gln	Gly	Asn	Cys	Leu	Ala	Ser	Asn	Gly	Ser	Thr	Ala	Leu	Met
			20					25					30		

Gly Glu Val Asp Met Gln Thr Pro Phe Pro Glu Trp Leu Thr Glu Phe  
 35 40 45  
 Thr Asn Leu Thr Gln Trp Pro Gly Ile Asp Pro Pro Tyr Ile Pro Leu  
 50 55 60  
 Asp Tyr Ile Asn Leu Thr Glu Val Pro Glu Leu Asp Arg Tyr Tyr Pro  
 65 70 75 80  
 Gly Gln Cys Pro Lys Ile Ser Arg Glu Gln Cys Ser Phe Asp Cys Tyr  
 85 90 95  
 Asn Cys Ile Asp Val Asp Asp Val Thr Ser Cys Phe Lys Leu Ser Gln  
 100 105 110  
 Thr Phe Asp Asp Gly Pro Ala Pro Ala Thr Glu Ala Leu Leu Lys Lys  
 115 120 125  
 Leu Arg Gln Arg Thr Thr Phe Phe Val Leu Gly Ile Asn Thr Val Asn  
 130 135 140  
 Tyr Pro Asp Ile Tyr Glu His Ile Leu Glu Arg Gly His Leu Ile Gly  
 145 150 155 160  
 Thr His Thr Trp Ser His Glu Phe Leu Pro Ser Leu Ser Asn Glu Glu  
 165 170 175  
 Ile Val Ala Gln Ile Glu Trp Ser Ile Trp Ala Met Asn Ala Thr Gly  
 180 185 190  
 Lys His Phe Pro Lys Tyr Phe Arg Pro Pro Tyr Gly Ala Ile Asp Asn  
 195 200 205  
 Arg Val Arg Ala Ile Val Lys Gln Phe Gly Leu Thr Val Val Leu Trp  
 210 215 220  
 Asp Leu Asp Thr Phe Asp Trp Lys Leu Ile Thr Asn Asp Asp Phe Arg  
 225 230 235 240  
 Thr Glu Glu Glu Ile Leu Met Asp Ile Asn Thr Trp Lys Gly Lys Arg  
 245 250 255  
 Lys Gly Leu Ile Leu Glu His Asp Gly Ala Arg Arg Thr Val Glu Val  
 260 265 270  
 Ala Ile Lys Ile Asn Glu Leu Ile Gly Ser Asp Gln Leu Thr Ile Ala  
 275 280 285

Glu Cys Ile Gly Asp Thr Asp Tyr Ile Glu Arg Tyr Asp  
 290 295 300

<210> 38  
 <211> 939  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> CDS  
 <222> (1)..(939)

<400> 38  
 atg aga ata caa cta aat aca att gat ttg caa tgt att att gca ctt 48  
 Met Arg Ile Gln Leu Asn Thr Ile Asp Leu Gln Cys Ile Ile Ala Leu  
 1 5 10 15  
 tcc tgt ctg ggg caa ttt gtt cac gcg gaa gct aat agg gaa gat tta 96  
 Ser Cys Leu Gly Gln Phe Val His Ala Glu Ala Asn Arg Glu Asp Leu  
 20 25 30  
 aag cag ata gac ttt caa ttt cct gta ttg gaa agg gca gct aca aaa 144  
 Lys Gln Ile Asp Phe Gln Phe Pro Val Leu Glu Arg Ala Ala Thr Lys  
 35 40 45  
 acg cct ttt ccg gat tgg ctt agt gca ttt acc ggg tta aaa gaa tgg 192  
 Thr Pro Phe Pro Asp Trp Leu Ser Ala Phe Thr Gly Leu Lys Glu Trp  
 50 55 60  
 cct ggg tta gat cca cct tat ata cct tta gat ttc att gat ttc agt 240  
 Pro Gly Leu Asp Pro Pro Tyr Ile Pro Leu Asp Phe Ile Asp Phe Ser  
 65 70 75 80  
 caa att cca gat tat aag gaa tat gat caa aac cat tgc gac agt gtt 288  
 Gln Ile Pro Asp Tyr Lys Glu Tyr Asp Gln Asn His Cys Asp Ser Val  
 85 90 95  
 cca agg gac tcg tgc tct ttc gat tgc cat cac tgc acc gaa cac gat 336  
 Pro Arg Asp Ser Cys Ser Phe Asp Cys His His Cys Thr Glu His Asp  
 100 105 110  
 gat gtg tac aca tgt tcc aaa ctt tcc cag aca ttt gac gat ggt cct 384  
 Asp Val Tyr Thr Cys Ser Lys Leu Ser Gln Thr Phe Asp Asp Gly Pro  
 115 120 125  
 tct gct tcc act act aaa tta ttg gac cgg ttg aag cat aat tcc acc 432  
 Ser Ala Ser Thr Thr Lys Leu Leu Asp Arg Leu Lys His Asn Ser Thr  
 130 135 140  
 ttc ttc aat tta ggt gtc aat ata gtt caa cat cca gat atc tat caa 480  
 Phe Phe Asn Leu Gly Val Asn Ile Val Gln His Pro Asp Ile Tyr Gln  
 145 150 155 160  
 aga atg caa aag gag gga cac tta atc ggc tca cat acc tgg tct cac 528  
 Arg Met Gln Lys Glu Gly His Leu Ile Gly Ser His Thr Trp Ser His  
 165 170 175  
 gta tat ttg cca aat gta tcg aat gaa aaa att ata gct caa att gaa 576  
 Val Tyr Leu Pro Asn Val Ser Asn Glu Lys Ile Ile Ala Gln Ile Glu

180	185	190	
tgg tcc atc tgg gcg atg aat gct act ggc aac cat acc ccc aaa tgg			624
Trp Ser Ile Trp Ala Met Asn Ala Thr Gly Asn His Thr Pro Lys Trp			
195	200	205	
ttc aga cct cca tat ggc gga ata gat aat aga gta aga gca ata aca			672
Phe Arg Pro Pro Tyr Gly Gly Ile Asp Asn Arg Val Arg Ala Ile Thr			
210	215	220	
agg caa ttt ggc tta caa gcc gtc tta tgg gat cac gat act ttt gat			720
Arg Gln Phe Gly Leu Gln Ala Val Leu Trp Asp His Asp Thr Phe Asp			
225	230	235	240
tgg agc ctc ctt ctc aat gat tct gtc ata act gaa caa gaa att ctt			768
Trp Ser Leu Leu Leu Asn Asp Ser Val Ile Thr Glu Gln Glu Ile Leu			
245	250	255	
caa aat gta ata aac tgg aac aag tca gga acc gga tta ata tta gaa			816
Gln Asn Val Ile Asn Trp Asn Lys Ser Gly Thr Gly Leu Ile Leu Glu			
260	265	270	
cac gat tca acg gaa aaa act gtc gat ctt gcc att aaa ata aat aag			864
His Asp Ser Thr Glu Lys Thr Val Asp Leu Ala Ile Lys Ile Asn Lys			
275	280	285	
ttg ata ggt gat gat caa tca aca gtt tct cat tgt gtc ggc gga att			912
Leu Ile Gly Asp Asp Gln Ser Thr Val Ser His Cys Val Gly Gly Ile			
290	295	300	
gat tac ata aaa gaa ttc ttg tcc taa			939
Asp Tyr Ile Lys Glu Phe Leu Ser			
305	310		

<210> 39  
 <211> 312  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 39

Met Arg Ile Gln Leu Asn Thr Ile Asp Leu Gln Cys Ile Ile Ala Leu
1 5 10 15

Ser Cys Leu Gly Gln Phe Val His Ala Glu Ala Asn Arg Glu Asp Leu
20 25 30

Lys Gln Ile Asp Phe Gln Phe Pro Val Leu Glu Arg Ala Ala Thr Lys
35 40 45

Thr Pro Phe Pro Asp Trp Leu Ser Ala Phe Thr Gly Leu Lys Glu Trp
50 55 60

Pro Gly Leu Asp Pro Pro Tyr Ile Pro Leu Asp Phe Ile Asp Phe Ser
65 70 75 80



Gln Ile Pro Asp Tyr Lys Glu Tyr Asp Gln Asn His Cys Asp Ser Val  
                     85                    90                    95

Pro Arg Asp Ser Cys Ser Phe Asp Cys His His Cys Thr Glu His Asp  
                     100                    105                    110

Asp Val Tyr Thr Cys Ser Lys Leu Ser Gln Thr Phe Asp Asp Gly Pro  
                     115                    120                    125

Ser Ala Ser Thr Thr Lys Leu Leu Asp Arg Leu Lys His Asn Ser Thr  
                     130                    135                    140

Phe Phe Asn Leu Gly Val Asn Ile Val Gln His Pro Asp Ile Tyr Gln  
 145                    150                    155                    160

Arg Met Gln Lys Glu Gly His Leu Ile Gly Ser His Thr Trp Ser His  
                     165                    170                    175

Val Tyr Leu Pro Asn Val Ser Asn Glu Lys Ile Ile Ala Gln Ile Glu  
                     180                    185                    190

Trp Ser Ile Trp Ala Met Asn Ala Thr Gly Asn His Thr Pro Lys Trp  
                     195                    200                    205

Phe Arg Pro Pro Tyr Gly Gly Ile Asp Asn Arg Val Arg Ala Ile Thr  
                     210                    215                    220

Arg Gln Phe Gly Leu Gln Ala Val Leu Trp Asp His Asp Thr Phe Asp  
 225                    230                    235                    240

Trp Ser Leu Leu Leu Asn Asp Ser Val Ile Thr Glu Gln Glu Ile Leu  
                     245                    250                    255

Gln Asn Val Ile Asn Trp Asn Lys Ser Gly Thr Gly Leu Ile Leu Glu  
                     260                    265                    270

His Asp Ser Thr Glu Lys Thr Val Asp Leu Ala Ile Lys Ile Asn Lys  
                     275                    280                    285

Leu Ile Gly Asp Asp Gln Ser Thr Val Ser His Cys Val Gly Gly Ile  
                     290                    295                    300

Asp Tyr Ile Lys Glu Phe Leu Ser  
 305                    310

<210> 40  
 <211> 2602

<212> DNA

<213> *Aspergillus niger*

<400> 40

ttcgtgcgct	aatgtctcgt	ccgttcacaa	actgaagagc	ttgaagtggc	gagatgtctc	60
tgcaggaatt	caagctagat	gctaagcgat	attgcatggc	aatatgtggt	gatgcatgtg	120
cttcttccct	cagcttcccc	tcgtgcgagt	gaggtttggc	tataaattga	agtggttggt	180
cggggttccg	tgaggggctg	aagtgccttc	tcccttttag	gcgcaactga	gagcctgagc	240
ttcatcccca	gcatcattac	acctcagcaa	tgctgctccg	atctctactc	gccctgagcg	300
gcctcgtctg	cacaggggtg	gcaaagtgtg	ttccaagcg	cgcgaccttg	gattcatggt	360
tgagcaacga	agcgaccgtg	gctcgtactg	ccatcctgaa	taacatcggg	gcggacgggtg	420
cttgggtgtc	gggcgcggac	tctggcattg	tcgttgctag	tcccagcacg	gataacccgg	480
actgtatggt	tcgagctcag	atttagtatg	agtgtgtcat	tgattgattg	atgctgactg	540
gcgtgtcgtt	tggtgtagac	ttctacacct	ggactcgcga	ctctgggtctc	gtcctcaaga	600
ccctcgtcga	tctcttccga	aatggagata	ccagtctcct	ctccaccatt	gagaactaca	660
tctccgcca	ggcaattgtc	cagggatatca	gtaacccctc	tggtgatctg	tccagcggcg	720
ctgggtctcg	tgaacccaag	ttcaatgtcg	atgagactgc	ctacactggg	tcttggggac	780
ggccgcagcg	agatgggtccg	gctctgagag	caactgctat	gatcggcttc	gggcagtggc	840
tgcttgtatg	ttctccaccc	ccttgcgctc	gatctgtgac	atatgtagct	gactgggtcag	900
gacaatggct	acaccagcac	cgcaacggac	attgtttggc	ccctcgttag	gaacgacctg	960
tcgtatgtgg	ctcaatactg	gaaccagaca	ggatatgggtg	tgtttgtttt	attttaaatt	1020
tccaaagatg	cgccagcaga	gctaaccocg	gatcgcagat	ctctgggaag	aagtcaatgg	1080
ctcgtctttc	tttacgattg	ctgtgcaaca	ccgcgccttc	gtcgaaggta	gtgccttcgc	1140
gacggccgtc	ggctcgtcct	gctcctgggtg	tgattctcag	gcacccgaaa	ttctctgcta	1200
cctgcagtcc	ttctggaccg	gcagcttcat	tctggccaac	ttcgatagca	gccgttccgg	1260
caaggacgca	aacaccctcc	tgggaagcat	ccacaccttt	gatcctgagg	ccgcatgcga	1320
cgactccacc	ttccagccct	gctccccgcg	cgcgctcgcc	aaccacaagg	aggttgtaga	1380
ctctttccgc	tcaatctata	ccctcaacga	tggtctcagt	gacagcgagg	ctgttgcggt	1440
gggtcggtag	cctgaggaca	cgtactacaa	cggcaaccocg	tggttcctgt	gcaccttggc	1500
tgccgcagag	cagttgtacg	atgctctata	ccagtgggac	aagcaggggt	cgttggaggt	1560
cacagatgtg	tcgctggact	tcttcaaggc	actgtacagc	gatgctgcta	ctggcaccta	1620
ctcttcgtcc	agttcgactt	atagtagcat	tgtagatgcc	gtgaagactt	tcgccgatgg	1680
cttcgtctct	attgtggtaa	gtctacgcta	gacaagcgct	catgttgaca	gaggggtcgt	1740

```

actaacagaa gtaggaaact cacgccgcaa gcaacggctc catgtccgag caatacgaca 1800
agttctgatgg cgagcagctt tccgctcgcg acctgacctg gtcttatgct gctctgctga 1860
ccgccaacaa ccgtcgtaac tccgtcgtgc ctgcttcttg gggcgagacc tctgccagca 1920
gcgtgccccg cacctgtgcg gccacatctg ccattggtac ctacagcagt gtgactgtca 1980
cctcgtggcc gagtatcgtg gctactggcg gcaccactac gacggctacc cccactggat 2040
ccggcagcgt gacctcgacc agcaagacca ccgcgactgc tagcaagacc agcaccagta 2100
cgtcacaaac ctctgtgacc actcccaccg ccgtggctgt gactttcgat ctgacagcta 2160
ccaccaccta cggcgagaac atctacctgg tcggatcgat ctctcagctg ggtgactggg 2220
aaaccagcga cggcatagct ctgagtgtg acaagtacac ttccagcgac ccgctctggt 2280
atgtcactgt gactctgccg gctgggtgagt cgtttgagta caagtttatc cgcattgaga 2340
gcgatgactc cgtggagtgg gagagtgatc ccaaccgaga atacaccgtt cctcaggcgt 2400
gcggaacgtc gaccgcgacg gtgactgaca cctggcggtg acaatcaatc catttcgcta 2460
tagttaaagg atggggatga gggcaattgg ttatatgatc atgtatgtag tgggtgtgca 2520
taatagtagt gaaatggaag ccaagtcatg tgattgtaat cgaccgacgg aattgaggat 2580
atccggaaat acagacaccg gg 2602

```

```

<210> 41
<211> 747
<212> DNA
<213> Candida albicans

```

```

<220>
<221> CDS
<222> (1)..(747)

```

```

<400> 41
atg aga caa gct ata ttt tcc aac cct aac gat gct gct gag tat ttg 48
Met Arg Gln Ala Ile Phe Ser Asn Pro Asn Asp Ala Ala Glu Tyr Leu
1 5 10 15

gca aac tat atc att gcc aaa atc aac tcc acc ccc aga aca ttt gtt 96
Ala Asn Tyr Ile Ile Ala Lys Ile Asn Ser Thr Pro Arg Thr Phe Val
20 25 30

ctt ggc ctt cca acc ggg tca tcc cct gaa ggc att tat gcc aaa ttg 144
Leu Gly Leu Pro Thr Gly Ser Ser Pro Glu Gly Ile Tyr Ala Lys Leu
35 40 45

atc gaa gcc aac aag caa ggc cgt gtt agt ttc aaa aac gtc gtg acc 192
Ile Glu Ala Asn Lys Gln Gly Arg Val Ser Phe Lys Asn Val Val Thr
50 55 60

ttc aac atg gac gag tat ttg gga ttt gcc cca tct gac ttg cag tcg 240
Phe Asn Met Asp Glu Tyr Leu Gly Phe Ala Pro Ser Asp Leu Gln Ser
65 70 75 80

```

tac cat tat ttc atg tac gac aag ttt ttc aac cat atc gat atc ccg	288
Tyr His Tyr Phe Met Tyr Asp Lys Phe Phe Asn His Ile Asp Ile Pro	
85 90 95	
cgT gaa aat atc cac atc ttg aac gga ttg gcc gca aac atc gac gag	336
Arg Glu Asn Ile His Ile Leu Asn Gly Leu Ala Ala Asn Ile Asp Glu	
100 105 110	
gag tgt gcc aac tac gaa aag aaa atc aag caa tac gga aga atc gat	384
Glu Cys Ala Asn Tyr Glu Lys Lys Ile Lys Gln Tyr Gly Arg Ile Asp	
115 120 125	
ttg ttc tta ggc ggg tta ggc cca gaa ggt cat ttg gca ttc aac gaa	432
Leu Phe Leu Leu Gly Gly Leu Gly Pro Glu Gly His Leu Ala Phe Asn Glu	
130 135 140	
gcg gga tca tca aga aac tca aaa aca aga aag gtc gag ttg gtc gaa	480
Ala Gly Ser Ser Arg Asn Ser Lys Thr Arg Lys Val Glu Leu Val Glu	
145 150 155 160	
agt acc atc aag gca aac tgc agg ttt ttc ggg aac gac gag agc aag	528
Ser Thr Ile Lys Ala Asn Cys Arg Phe Phe Gly Asn Asp Glu Ser Lys	
165 170 175	
gtc cct aaa tat gca ttg agt gtt ggt att tcc acc atc ttg gac aac	576
Val Pro Lys Tyr Ala Leu Ser Val Gly Ile Ser Thr Ile Leu Asp Asn	
180 185 190	
tca gac gaa att gcc att atc gtg ttg ggc aaa agt aaa caa ttt gca	624
Ser Asp Glu Ile Ala Ile Ile Val Leu Gly Lys Ser Lys Gln Phe Ala	
195 200 205	
ttg gac aaa act gta aac ggg aaa cca aac gac cca aaa tac cca tca	672
Leu Asp Lys Thr Val Asn Gly Lys Pro Asn Asp Pro Lys Tyr Pro Ser	
210 215 220	
agc tat tta caa gac cac gca aat gtc ttg att gtt tgc gat aac gct	720
Ser Tyr Leu Gln Asp His Ala Asn Val Leu Val Val Cys Asp Asn Ala	
225 230 235 240	
gcc gct gga tta aag tca aag ttg tag	747
Ala Ala Gly Leu Lys Ser Lys Leu	
245	

<210> 42  
 <211> 248  
 <212> PRT  
 <213> Candida albicans

<400> 42

Met Arg Gln Ala Ile Phe Ser Asn Pro Asn Asp Ala Ala Glu Tyr Leu
1 5 10 15

Ala Asn Tyr Ile Ile Ala Lys Ile Asn Ser Thr Pro Arg Thr Phe Val
20 25 30

Leu Gly Leu Pro Thr Gly Ser Ser Pro Glu Gly Ile Tyr Ala Lys Leu
35 40 45

Ile Glu Ala Asn Lys Gln Gly Arg Val Ser Phe Lys Asn Val Val Thr  
 50 55 60  
 Phe Asn Met Asp Glu Tyr Leu Gly Phe Ala Pro Ser Asp Leu Gln Ser  
 65 70 75 80  
 Tyr His Tyr Phe Met Tyr Asp Lys Phe Phe Asn His Ile Asp Ile Pro  
 85 90 95  
 Arg Glu Asn Ile His Ile Leu Asn Gly Leu Ala Ala Asn Ile Asp Glu  
 100 105 110  
 Glu Cys Ala Asn Tyr Glu Lys Lys Ile Lys Gln Tyr Gly Arg Ile Asp  
 115 120 125  
 Leu Phe Leu Gly Gly Leu Gly Pro Glu Gly His Leu Ala Phe Asn Glu  
 130 135 140  
 Ala Gly Ser Ser Arg Asn Ser Lys Thr Arg Lys Val Glu Leu Val Glu  
 145 150 155 160  
 Ser Thr Ile Lys Ala Asn Cys Arg Phe Phe Gly Asn Asp Glu Ser Lys  
 165 170 175  
 Val Pro Lys Tyr Ala Leu Ser Val Gly Ile Ser Thr Ile Leu Asp Asn  
 180 185 190  
 Ser Asp Glu Ile Ala Ile Ile Val Leu Gly Lys Ser Lys Gln Phe Ala  
 195 200 205  
 Leu Asp Lys Thr Val Asn Gly Lys Pro Asn Asp Pro Lys Tyr Pro Ser  
 210 215 220  
 Ser Tyr Leu Gln Asp His Ala Asn Val Leu Ile Val Cys Asp Asn Ala  
 225 230 235 240  
 Ala Ala Gly Leu Lys Ser Lys Leu  
 245

<210> 43  
 <211> 721  
 <212> DNA  
 <213> Candida albicans

<400> 43  
 ttacggtgat gtggctgtgg catggcattg taccaagtgt gtgatcatcg tagcaccttt 60  
 ctcaacagct ttcacggctg tgcataatc cgacatcgta tggccaatgg aaaacacaca 120

gttcttggat ttaacaacag gtatcaagtc taaaacacca gcaatttcag gagcagcagt 180  
 gacaatacac acattatcaa acaagtcccc gtaaacttct aacaattttg attcaccctc 240  
 tttggcatca acaaacgttt cgactgggtg gcaccctttc ttttgacat tgataaatgg 300  
 cgcctcactg agctccagcg aatctgtctg acttgccaaa acactcctct tgtacattgg 360  
 caacactttg gcatacactt ctgggaagct tgatgtgaca gtaggacacg tagcagtaac 420  
 cccagtactc aaatacttgg ccatagcatc tctatagaac cgcttaaact cagcaacatc 480  
 ctctgcggta gactcctcgc caagattgga aaagttcaac ccataaatac cgttattctg 540  
 aatatcaata aaccaggtg ctaatatattg ctgcttcaaa tctataacct cactaaccaa 600  
 ctcagggttt gctggcggat gacaaattct tttggtggcg ttgttgacgt acaagtcagt 660  
 aaactcatac aactcaccgt tgtcgatcaa atgacagttt gtgaatctag taaatgacat 720  
 g 721

<210> 44  
 <211> 239  
 <212> PRT  
 <213> Candida albicans

<400> 44

Met Ser Phe Thr Arg Phe Thr Asn Cys His Leu Ile Asp Asn Gly Glu  
 1 5 10 15

Leu Tyr Glu Phe Thr Asp Leu Tyr Val Asn Asn Ala Thr Lys Arg Ile  
 20 25 30

Cys His Pro Pro Ala Asn Pro Glu Leu Val Ser Glu Val Ile Asp Leu  
 35 40 45

Lys Gln Gln Ile Leu Ala Pro Gly Phe Ile Asp Ile Gln Asn Asn Gly  
 50 55 60

Ile Tyr Gly Leu Asn Phe Ser Asn Leu Gly Glu Glu Ser Thr Ala Glu  
 65 70 75 80

Asp Val Ala Glu Phe Lys Arg Phe Tyr Arg Asp Ala Met Ala Lys Tyr  
 85 90 95

Leu Ser Thr Gly Val Thr Ala Thr Cys Pro Thr Val Thr Ser Ser Phe  
 100 105 110

Pro Glu Val Tyr Ala Lys Val Leu Pro Met Tyr Lys Arg Ser Val Leu  
 115 120 125

Ala Ser Gln Thr Asp Ser Ser Glu Leu Ser Glu Ala Pro Phe Ile Asn  
130 135 140

Val Gln Lys Lys Gly Cys His Pro Val Glu Thr Phe Val Asp Ala Lys  
145 150 155 160

Glu Gly Glu Ser Lys Leu Leu Glu Val Tyr Gly Asp Leu Phe Asp Asn  
165 170 175

Val Cys Ile Val Thr Ala Ala Pro Glu Ile Ala Gly Val Leu Asp Leu  
180 185 190

Ile Pro Val Val Lys Ser Lys Asn Cys Val Phe Ser Ile Gly His Thr  
195 200 205

Met Ser Asp Tyr Asp Thr Ala Val Lys Ala Val Glu Lys Gly Ala Thr  
210 215 220

Met Ile Thr His Leu Val Gln Cys His Ala Thr Ala Thr Ser Pro  
225 230 235

<210> 45  
<211> 3396  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)..(3396)

<400> 45  
atg agt gat caa aat aat cga tcg aga aat gaa tat cac tca aac cgg 48  
Met Ser Asp Gln Asn Asn Arg Ser Arg Asn Glu Tyr His Ser Asn Arg  
1 5 10 15  
aag aat gaa cct tcc tat gaa ctc caa aat gca cat agc ggg cta ttt 96  
Lys Asn Glu Pro Ser Tyr Glu Leu Gln Asn Ala His Ser Gly Leu Phe  
20 25 30  
cac tct tct aat gaa gaa tta aca aac agg aac caa aga tat acc aat 144  
His Ser Ser Asn Glu Glu Leu Thr Asn Arg Asn Gln Arg Tyr Thr Asn  
35 40 45  
caa aat gcc agc atg ggt tca ttc act cca gtc caa tct ttg caa ttt 192  
Gln Asn Ala Ser Met Gly Ser Phe Thr Pro Val Gln Ser Leu Gln Phe  
50 55 60  
cca gaa caa tct cag caa aca aat atg ctt tat aac ggt gac gat ggc 240  
Pro Glu Gln Ser Gln Gln Thr Asn Met Leu Tyr Asn Gly Asp Asp Gly  
65 70 75 80  
aat aat aat act atc aat gat aac gaa cga gac ata tat gga ggt ttt 288  
Asn Asn Asn Thr Ile Asn Asp Asn Glu Arg Asp Ile Tyr Gly Gly Phe  
85 90 95

gtc aac cac cat cgc cag cgt ccc cca cca gca act gca gaa tac aat	336
Val Asn His His Arg Gln Arg Pro Pro Pro Ala Thr Ala Glu Tyr Asn	
100 105 110	
gac gtt ttt aat acg aat agt caa cag cta ccg tcg gaa cat caa tac	384
Asp Val Phe Asn Thr Asn Ser Gln Gln Leu Pro Ser Glu His Gln Tyr	
115 120 125	
aat aac gta cct tca tat cca ctt cct tcg ata aat gtg att caa acc	432
Asn Asn Val Pro Ser Tyr Pro Leu Pro Ser Ile Asn Val Ile Gln Thr	
130 135 140	
act cca gaa ctc ata cat aac ggc tca cag act atg gcc acc ccc atc	480
Thr Pro Glu Leu Ile His Asn Gly Ser Gln Thr Met Ala Thr Pro Ile	
145 150 155 160	
gaa agg ccc ttc ttt aac gaa aac gac tac tat tat aat aac agg aac	528
Glu Arg Pro Phe Phe Asn Glu Asn Asp Tyr Tyr Tyr Asn Asn Arg Asn	
165 170 175	
tct agg acg tca ccg agt att gct tct agt agc gat ggt tat gca gat	576
Ser Arg Thr Ser Pro Ser Ile Ala Ser Ser Ser Asp Gly Tyr Ala Asp	
180 185 190	
cag gaa gct agg ccc att ttg gag caa ccc aac aat aac atg aat agc	624
Gln Glu Ala Arg Pro Ile Leu Glu Gln Pro Asn Asn Asn Met Asn Ser	
195 200 205	
ggt aat att cct caa tac cat gac caa cct ttt gga tac aac aat ggt	672
Gly Asn Ile Pro Gln Tyr His Asp Gln Pro Phe Gly Tyr Asn Asn Gly	
210 215 220	
tac cat ggc cta cag gca aaa gat tac tat gac gat ccg gag ggt ggt	720
Tyr His Gly Leu Gln Ala Lys Asp Tyr Tyr Asp Asp Pro Glu Gly Gly	
225 230 235 240	
tat att gat cag aga gga gat gac tat cag att aat tca tat ttg ggt	768
Tyr Ile Asp Gln Arg Gly Asp Asp Tyr Gln Ile Asn Ser Tyr Leu Gly	
245 250 255	
aga aac ggt gaa atg gtt gat cct tac gat tat gaa aac agt tta aga	816
Arg Asn Gly Glu Met Val Asp Pro Tyr Asp Tyr Glu Asn Ser Leu Arg	
260 265 270	
cat atg act cct atg gag cgt aga gaa tat ctt cat gat gat agc aga	864
His Met Thr Pro Met Glu Arg Arg Glu Tyr Leu His Asp Asp Ser Arg	
275 280 285	
ccc gta aac gat gga aaa gaa gaa tta gac agt gtg aaa agc ggt tac	912
Pro Val Asn Asp Gly Lys Glu Glu Leu Asp Ser Val Lys Ser Gly Tyr	
290 295 300	
tct cat aga gac ttg ggg gaa tat gac aag gat gat ttt tca agg gat	960
Ser His Arg Asp Leu Gly Glu Tyr Asp Lys Asp Asp Phe Ser Arg Asp	
305 310 315 320	
gac gag tac gat gat ctc aac act att gat aaa tta cag ttt caa gct	1008
Asp Glu Tyr Asp Asp Leu Asn Thr Ile Asp Lys Leu Gln Phe Gln Ala	
325 330 335	
aat ggt gta cct gca tca tcc tcg gtg tct tct atc gga tct aaa gaa	1056
Asn Gly Val Pro Ala Ser Ser Ser Val Ser Ser Ile Gly Ser Lys Glu	



340	345	350	
tcc gac ata ata gta agc aat gat aac tta acc gca aat aga gca cta Ser Asp Ile Ile Val Ser Asn Asp Asn Leu Thr Ala Asn Arg Ala Leu 355 360 365			1104
aag aga agc ggt act gaa att agg aaa ttc aaa ctt tgg aat ggt aat Lys Arg Ser Gly Thr Glu Ile Arg Lys Phe Lys Leu Trp Asn Gly Asn 370 375 380			1152
ttt gtt ttc gat tct cca atc agt aag acg cta ttg gac caa tac gct Phe Val Phe Asp Ser Pro Ile Ser Lys Thr Leu Leu Asp Gln Tyr Ala 385 390 395 400			1200
act aca aca gaa aat gca aac act tta cca aat gag ttt aag ttt atg Thr Thr Thr Glu Asn Ala Asn Thr Leu Pro Asn Glu Phe Lys Phe Met 405 410 415			1248
aga tat caa gca gtt act tgc gaa cct aat caa ctt gca gag aag aat Arg Tyr Gln Ala Val Thr Cys Glu Pro Asn Gln Leu Ala Glu Lys Asn 420 425 430			1296
ttc acg gtg agg cag ttg aag tat tta act cca agg gaa acg gaa ttg Phe Thr Val Arg Gln Leu Lys Tyr Leu Thr Pro Arg Glu Thr Glu Leu 435 440 445			1344
atg cta gta gtc aca atg tat aat gaa gac cat atc ctg tta gga aga Met Leu Val Val Thr Met Tyr Asn Glu Asp His Ile Leu Leu Gly Arg 450 455 460			1392
act ttg aaa ggt att atg gac aat gtc aaa tat atg gtg aaa aaa aaa Thr Leu Lys Gly Ile Met Asp Asn Val Lys Tyr Met Val Lys Lys Lys 465 470 475 480			1440
aat tca agc act tgg ggg ccg gat gca tgg aaa aag att gtc gtt tgt Asn Ser Ser Thr Trp Gly Pro Asp Ala Trp Lys Lys Ile Val Val Cys 485 490 495			1488
atc att tca gat ggt aga tcc aaa att aat gaa cgc tcg cta gca tta Ile Ile Ser Asp Gly Arg Ser Lys Ile Asn Glu Arg Ser Leu Ala Leu 500 505 510			1536
cta agt tcg tta ggt tgt tac cag gac ggg ttt gct aag gat gaa att Leu Ser Ser Leu Gly Cys Tyr Gln Asp Gly Phe Ala Lys Asp Glu Ile 515 520 525			1584
aat gaa aaa aaa gtg gca atg cat gtc tac gaa cat acg aca atg atc Asn Glu Lys Lys Val Ala Met His Val Tyr Glu His Thr Thr Met Ile 530 535 540			1632
aac atc aca aat att tcg gaa tca gag gtt tca tta gaa tgc aat caa Asn Ile Thr Asn Ile Ser Glu Ser Glu Val Ser Leu Glu Cys Asn Gln 545 550 555 560			1680
ggt acc gtt cca ata caa ctt ttg ttt tgt ttg aaa gag caa aat cag Gly Thr Val Pro Ile Gln Leu Leu Phe Cys Leu Lys Glu Gln Asn Gln 565 570 575			1728
aaa aaa att aac tca cat aga tgg gca ttt gaa ggc ttt gca gaa tta Lys Lys Ile Asn Ser His Arg Trp Ala Phe Glu Gly Phe Ala Glu Leu 580 585 590			1776

ctg cgt ccc aat atc gtt aca ttg tta gat gct ggt acc atg cca ggt	1824
Leu Arg Pro Asn Ile Val Thr Leu Leu Asp Ala Gly Thr Met Pro Gly	
595 600 605	
aaa gat tct att tac cag tta tgg aga gag ttc agg aat cca aat gtt	1872
Lys Asp Ser Ile Tyr Gln Leu Trp Arg Glu Phe Arg Asn Pro Asn Val	
610 615 620	
ggt ggc gca tgt ggt gaa ata aga act gat ttg ggt aag aga ttt gta	1920
Gly Gly Ala Cys Gly Glu Ile Arg Thr Asp Leu Gly Lys Arg Phe Val	
625 630 635 640	
aag ctt ttg aat cct tta gtt gca tca cag aat ttc gaa tac aaa atg	1968
Lys Leu Leu Asn Pro Leu Val Ala Ser Gln Asn Phe Glu Tyr Lys Met	
645 650 655	
tcc aat att tta gac aaa aca acc gag tct aac ttt gga ttt att act	2016
Ser Asn Ile Leu Asp Lys Thr Thr Glu Ser Asn Phe Gly Phe Ile Thr	
660 665 670	
gtt cta ccg ggg gca ttc tct gcg tat agg ttt gaa gct gtg aga ggc	2064
Val Leu Pro Gly Ala Phe Ser Ala Tyr Arg Phe Glu Ala Val Arg Gly	
675 680 685	
caa cca tta cag aag tac ttt tat ggt gaa att atg gaa aat gaa ggc	2112
Gln Pro Leu Gln Lys Tyr Phe Tyr Gly Glu Ile Met Glu Asn Glu Gly	
690 695 700	
ttt cat ttt ttt tct tcc aat atg tat ctt gct gaa gat cgt att tta	2160
Phe His Phe Phe Ser Ser Asn Met Tyr Leu Ala Glu Asp Arg Ile Leu	
705 710 715 720	
tgc ttt gaa gtg gtc aca aaa aaa aat tgt aat tgg att ttg aaa tac	2208
Cys Phe Glu Val Val Thr Lys Lys Asn Cys Asn Trp Ile Leu Lys Tyr	
725 730 735	
tgc aga agt tct tat gct tca aca gat gta ccg gag agg gtc cct gaa	2256
Cys Arg Ser Ser Tyr Ala Ser Thr Asp Val Pro Glu Arg Val Pro Glu	
740 745 750	
ttt att ctt cag agg agg cgt tgg ttg aat ggt tca ttt ttt gct agt	2304
Phe Ile Leu Gln Arg Arg Arg Trp Leu Asn Gly Ser Phe Phe Ala Ser	
755 760 765	
gta tat tcc ttt tgt cat ttt tac aga gtc tgg agc agt ggt cat aat	2352
Val Tyr Ser Phe Cys His Phe Tyr Arg Val Trp Ser Ser Gly His Asn	
770 775 780	
att ggt aga aaa ctc ctt ttg acg gtt gaa ttt ttt tac ctt ttc ttc	2400
Ile Gly Arg Lys Leu Leu Leu Thr Val Glu Phe Phe Tyr Leu Phe Phe	
785 790 795 800	
aat aca ttg att tca tgg ttt tca ttg agt tca ttt ttc cta ttc ttt	2448
Asn Thr Leu Ile Ser Trp Phe Ser Leu Ser Ser Phe Phe Leu Phe Phe	
805 810 815	
aga att ctc act gtt tct att gca ctg gca tac cat tca gca ttt aat	2496
Arg Ile Leu Thr Val Ser Ile Ala Leu Ala Tyr His Ser Ala Phe Asn	
820 825 830	
gtg ttg tcc gtc ata ttc ctg tgg ctt tat ggg att tgt acc tta tca	2544
Val Leu Ser Val Ile Phe Leu Trp Leu Tyr Gly Ile Cys Thr Leu Ser	

835	840	845	
aca ttc ata ctg tca ttg ggt aat aaa cct aaa agt act gag aaa ttt			2592
Thr Phe Ile Leu Ser Leu Gly Asn Lys Pro Lys Ser Thr Glu Lys Phe			
850	855	860	
tat gtt cta act tgc gtc att ttt gcg gtg atg atg att tac atg ata			2640
Tyr Val Leu Thr Cys Val Ile Phe Ala Val Met Met Ile Tyr Met Ile			
865	870	875 880	
ttc tgc agt ata ttc atg agt gtc aaa tcc ttc caa aat ata ttg aaa			2688
Phe Cys Ser Ile Phe Met Ser Val Lys Ser Phe Gln Asn Ile Leu Lys			
885	890	895	
aac gat acc atc agc ttt gag ggt ttg att acc aca gaa gct ttc agg			2736
Asn Asp Thr Ile Ser Phe Glu Gly Leu Ile Thr Thr Glu Ala Phe Arg			
900	905	910	
gat att gtt atc tct ctg ggc tcc act tat tgt ttg tac cta atc agt			2784
Asp Ile Val Ile Ser Leu Gly Ser Thr Tyr Cys Leu Tyr Leu Ile Ser			
915	920	925	
tca att atc tat ttg cag cca tgg cat atg ttg aca agt ttt att cag			2832
Ser Ile Ile Tyr Leu Gln Pro Trp His Met Leu Thr Ser Phe Ile Gln			
930	935	940	
tat att tta ttg agt cct tct tac atc aat gtt ttg aat atc tat gca			2880
Tyr Ile Leu Leu Ser Pro Ser Tyr Ile Asn Val Leu Asn Ile Tyr Ala			
945	950	955 960	
ttt tgt aat gtc cac gac tta tca tgg ggt aca aag ggt gca atg gca			2928
Phe Cys Asn Val His Asp Leu Ser Trp Gly Thr Lys Gly Ala Met Ala			
965	970	975	
aat ccg ctg ggt aag att aat act aca gaa gat ggt acg ttc aaa atg			2976
Asn Pro Leu Gly Lys Ile Asn Thr Thr Glu Asp Gly Thr Phe Lys Met			
980	985	990	
gaa gtt ctg gtc tct agt tca gag att caa gca aac tac gat aaa tat			3024
Glu Val Leu Val Ser Ser Ser Glu Ile Gln Ala Asn Tyr Asp Lys Tyr			
995	1000	1005	
ttg aaa gtt tta aat gac ttc gat cca aaa tca gaa tct cgg cct			3069
Leu Lys Val Leu Asn Asp Phe Asp Pro Lys Ser Glu Ser Arg Pro			
1010	1015	1020	
act gag cca tct tat gat gaa aaa aag act ggc tat tat gca aac			3114
Thr Glu Pro Ser Tyr Asp Glu Lys Lys Thr Gly Tyr Tyr Ala Asn			
1025	1030	1035	
gtt aga tct ctc gtg att atc ttt tgg gtc atc aca aat ttc atc			3159
Val Arg Ser Leu Val Ile Ile Phe Trp Val Ile Thr Asn Phe Ile			
1040	1045	1050	
atc gtt gct gtt gtc tta gaa acc ggt ggg att gca gat tat att			3204
Ile Val Ala Val Val Leu Glu Thr Gly Gly Ile Ala Asp Tyr Ile			
1055	1060	1065	
gct atg aaa tcc ata tca act gat gac act tta gaa act gca aag			3249
Ala Met Lys Ser Ile Ser Thr Asp Asp Thr Leu Glu Thr Ala Lys			
1070	1075	1080	

aag gcg gaa att ccc tta atg acc agt aag gcc tca att tat ttt 3294  
 Lys Ala Glu Ile Pro Leu Met Thr Ser Lys Ala Ser Ile Tyr Phe  
 1085 1090 1095

aat gta att tta tgg tta gtt gca tta tcg gca tta ata agg ttc 3339  
 Asn Val Ile Leu Trp Leu Val Ala Leu Ser Ala Leu Ile Arg Phe  
 1100 1105 1110

att ggt tgc tca ata tac atg ata gta agg ttt ttt aaa aag gtt 3384  
 Ile Gly Cys Ser Ile Tyr Met Ile Val Arg Phe Phe Lys Lys Val  
 1115 1120 1125

aca ttt cgc taa 3396  
 Thr Phe Arg  
 1130

<210> 46  
 <211> 1131  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 46

Met Ser Asp Gln Asn Asn Arg Ser Arg Asn Glu Tyr His Ser Asn Arg  
 1 5 10 15

Lys Asn Glu Pro Ser Tyr Glu Leu Gln Asn Ala His Ser Gly Leu Phe  
 20 25 30

His Ser Ser Asn Glu Glu Leu Thr Asn Arg Asn Gln Arg Tyr Thr Asn  
 35 40 45

Gln Asn Ala Ser Met Gly Ser Phe Thr Pro Val Gln Ser Leu Gln Phe  
 50 55 60

Pro Glu Gln Ser Gln Gln Thr Asn Met Leu Tyr Asn Gly Asp Asp Gly  
 65 70 75 80

Asn Asn Asn Thr Ile Asn Asp Asn Glu Arg Asp Ile Tyr Gly Gly Phe  
 85 90 95

Val Asn His His Arg Gln Arg Pro Pro Pro Ala Thr Ala Glu Tyr Asn  
 100 105 110

Asp Val Phe Asn Thr Asn Ser Gln Gln Leu Pro Ser Glu His Gln Tyr  
 115 120 125

Asn Asn Val Pro Ser Tyr Pro Leu Pro Ser Ile Asn Val Ile Gln Thr  
 130 135 140

Thr Pro Glu Leu Ile His Asn Gly Ser Gln Thr Met Ala Thr Pro Ile  
 145 150 155 160

Glu Arg Pro Phe Phe Asn Glu Asn Asp Tyr Tyr Tyr Asn Asn Arg Asn  
 165 170 175

Ser Arg Thr Ser Pro Ser Ile Ala Ser Ser Ser Asp Gly Tyr Ala Asp  
 180 185 190

Gln Glu Ala Arg Pro Ile Leu Glu Gln Pro Asn Asn Asn Met Asn Ser  
 195 200 205

Gly Asn Ile Pro Gln Tyr His Asp Gln Pro Phe Gly Tyr Asn Asn Gly  
 210 215 220

Tyr His Gly Leu Gln Ala Lys Asp Tyr Tyr Asp Asp Pro Glu Gly Gly  
 225 230 235 240

Tyr Ile Asp Gln Arg Gly Asp Asp Tyr Gln Ile Asn Ser Tyr Leu Gly  
 245 250 255

Arg Asn Gly Glu Met Val Asp Pro Tyr Asp Tyr Glu Asn Ser Leu Arg  
 260 265 270

His Met Thr Pro Met Glu Arg Arg Glu Tyr Leu His Asp Asp Ser Arg  
 275 280 285

Pro Val Asn Asp Gly Lys Glu Glu Leu Asp Ser Val Lys Ser Gly Tyr  
 290 295 300

Ser His Arg Asp Leu Gly Glu Tyr Asp Lys Asp Asp Phe Ser Arg Asp  
 305 310 315 320

Asp Glu Tyr Asp Asp Leu Asn Thr Ile Asp Lys Leu Gln Phe Gln Ala  
 325 330 335

Asn Gly Val Pro Ala Ser Ser Ser Val Ser Ser Ile Gly Ser Lys Glu  
 340 345 350

Ser Asp Ile Ile Val Ser Asn Asp Asn Leu Thr Ala Asn Arg Ala Leu  
 355 360 365

Lys Arg Ser Gly Thr Glu Ile Arg Lys Phe Lys Leu Trp Asn Gly Asn  
 370 375 380

Phe Val Phe Asp Ser Pro Ile Ser Lys Thr Leu Leu Asp Gln Tyr Ala  
 385 390 395 400

Thr Thr Thr Glu Asn Ala Asn Thr Leu Pro Asn Glu Phe Lys Phe Met

				405				410				415			
Arg	Tyr	Gln	Ala	Val	Thr	Cys	Glu	Pro	Asn	Gln	Leu	Ala	Glu	Lys	Asn
			420				425						430		
Phe	Thr	Val	Arg	Gln	Leu	Lys	Tyr	Leu	Thr	Pro	Arg	Glu	Thr	Glu	Leu
		435				440						445			
Met	Leu	Val	Val	Thr	Met	Tyr	Asn	Glu	Asp	His	Ile	Leu	Leu	Gly	Arg
		450				455				460					
Thr	Leu	Lys	Gly	Ile	Met	Asp	Asn	Val	Lys	Tyr	Met	Val	Lys	Lys	Lys
465				470						475				480	
Asn	Ser	Ser	Thr	Trp	Gly	Pro	Asp	Ala	Trp	Lys	Lys	Ile	Val	Val	Cys
			485				490						495		
Ile	Ile	Ser	Asp	Gly	Arg	Ser	Lys	Ile	Asn	Glu	Arg	Ser	Leu	Ala	Leu
			500				505						510		
Leu	Ser	Ser	Leu	Gly	Cys	Tyr	Gln	Asp	Gly	Phe	Ala	Lys	Asp	Glu	Ile
		515				520						525			
Asn	Glu	Lys	Lys	Val	Ala	Met	His	Val	Tyr	Glu	His	Thr	Thr	Met	Ile
		530				535				540					
Asn	Ile	Thr	Asn	Ile	Ser	Glu	Ser	Glu	Val	Ser	Leu	Glu	Cys	Asn	Gln
545				550						555				560	
Gly	Thr	Val	Pro	Ile	Gln	Leu	Leu	Phe	Cys	Leu	Lys	Glu	Gln	Asn	Gln
			565				570						575		
Lys	Lys	Ile	Asn	Ser	His	Arg	Trp	Ala	Phe	Glu	Gly	Phe	Ala	Glu	Leu
			580				585						590		
Leu	Arg	Pro	Asn	Ile	Val	Thr	Leu	Leu	Asp	Ala	Gly	Thr	Met	Pro	Gly
		595				600						605			
Lys	Asp	Ser	Ile	Tyr	Gln	Leu	Trp	Arg	Glu	Phe	Arg	Asn	Pro	Asn	Val
		610				615				620					
Gly	Gly	Ala	Cys	Gly	Glu	Ile	Arg	Thr	Asp	Leu	Gly	Lys	Arg	Phe	Val
625				630						635				640	
Lys	Leu	Leu	Asn	Pro	Leu	Val	Ala	Ser	Gln	Asn	Phe	Glu	Tyr	Lys	Met
			645				650						655		

Ser Asn Ile Leu Asp Lys Thr Thr Glu Ser Asn Phe Gly Phe Ile Thr  
 660 665 670

Val Leu Pro Gly Ala Phe Ser Ala Tyr Arg Phe Glu Ala Val Arg Gly  
 675 680 685

Gln Pro Leu Gln Lys Tyr Phe Tyr Gly Glu Ile Met Glu Asn Glu Gly  
 690 695 700

Phe His Phe Phe Ser Ser Asn Met Tyr Leu Ala Glu Asp Arg Ile Leu  
 705 710 715 720

Cys Phe Glu Val Val Thr Lys Lys Asn Cys Asn Trp Ile Leu Lys Tyr  
 725 730 735

Cys Arg Ser Ser Tyr Ala Ser Thr Asp Val Pro Glu Arg Val Pro Glu  
 740 745 750

Phe Ile Leu Gln Arg Arg Arg Trp Leu Asn Gly Ser Phe Phe Ala Ser  
 755 760 765

Val Tyr Ser Phe Cys His Phe Tyr Arg Val Trp Ser Ser Gly His Asn  
 770 775 780

Ile Gly Arg Lys Leu Leu Leu Thr Val Glu Phe Phe Tyr Leu Phe Phe  
 785 790 795 800

Asn Thr Leu Ile Ser Trp Phe Ser Leu Ser Ser Phe Phe Leu Phe Phe  
 805 810 815

Arg Ile Leu Thr Val Ser Ile Ala Leu Ala Tyr His Ser Ala Phe Asn  
 820 825 830

Val Leu Ser Val Ile Phe Leu Trp Leu Tyr Gly Ile Cys Thr Leu Ser  
 835 840 845

Thr Phe Ile Leu Ser Leu Gly Asn Lys Pro Lys Ser Thr Glu Lys Phe  
 850 855 860

Tyr Val Leu Thr Cys Val Ile Phe Ala Val Met Met Ile Tyr Met Ile  
 865 870 875 880

Phe Cys Ser Ile Phe Met Ser Val Lys Ser Phe Gln Asn Ile Leu Lys  
 885 890 895

Asn Asp Thr Ile Ser Phe Glu Gly Leu Ile Thr Thr Glu Ala Phe Arg  
 900 905 910

Asp Ile Val Ile Ser Leu Gly Ser Thr Tyr Cys Leu Tyr Leu Ile Ser  
915 920 925

Ser Ile Ile Tyr Leu Gln Pro Trp His Met Leu Thr Ser Phe Ile Gln  
930 935 940

Tyr Ile Leu Leu Ser Pro Ser Tyr Ile Asn Val Leu Asn Ile Tyr Ala  
945 950 955 960

Phe Cys Asn Val His Asp Leu Ser Trp Gly Thr Lys Gly Ala Met Ala  
965 970 975

Asn Pro Leu Gly Lys Ile Asn Thr Thr Glu Asp Gly Thr Phe Lys Met  
980 985 990

Glu Val Leu Val Ser Ser Ser Glu Ile Gln Ala Asn Tyr Asp Lys Tyr  
995 1000 1005

Leu Lys Val Leu Asn Asp Phe Asp Pro Lys Ser Glu Ser Arg Pro  
1010 1015 1020

Thr Glu Pro Ser Tyr Asp Glu Lys Lys Thr Gly Tyr Tyr Ala Asn  
1025 1030 1035

Val Arg Ser Leu Val Ile Ile Phe Trp Val Ile Thr Asn Phe Ile  
1040 1045 1050

Ile Val Ala Val Val Leu Glu Thr Gly Gly Ile Ala Asp Tyr Ile  
1055 1060 1065

Ala Met Lys Ser Ile Ser Thr Asp Asp Thr Leu Glu Thr Ala Lys  
1070 1075 1080

Lys Ala Glu Ile Pro Leu Met Thr Ser Lys Ala Ser Ile Tyr Phe  
1085 1090 1095

Asn Val Ile Leu Trp Leu Val Ala Leu Ser Ala Leu Ile Arg Phe  
1100 1105 1110

Ile Gly Cys Ser Ile Tyr Met Ile Val Arg Phe Phe Lys Lys Val  
1115 1120 1125

Thr Phe Arg  
1130

<210> 47



<211> 189  
 <212> PRT  
 <213> Aspergillus niger

<220>  
 <221> misc\_feature  
 <222> (1)..(189)  
 <223> Xaa = any amino acid

<400> 47

Asp Phe Leu Phe Ala Arg Thr Met Ile Gly Val Phe Lys Asn Ile Glu  
 1 5 10 15

Tyr Met Cys Ser Arg Thr Ser Ser Lys Thr Trp Gly Lys Asp Ala Trp  
 20 25 30

Lys Lys Ile Val Val Cys Val Ile Ser Asp Gly Arg Ala Lys Ile Asn  
 35 40 45

Pro Arg Thr Arg Ala Val Leu Ala Gly Leu Gly Cys Tyr Gln Asp Gly  
 50 55 60

Ile Ala Lys Gln Gln Val Asn Gly Lys Asp Val Thr Ala His Ile Tyr  
 65 70 75 80

Glu Tyr Thr Thr Gln Val Gly Leu Glu Leu Lys Gly Gly Gln Val Ser  
 85 90 95

Leu Lys Pro Arg Thr Gly Cys Pro Val Gln Met Ile Phe Cys Leu Lys  
 100 105 110

Glu Lys Asn Gln Lys Lys Ile Asn Ser His Arg Trp Phe Phe Gln Ala  
 115 120 125

Phe Gly Arg Val Leu Asp Pro Asn Ile Cys Val Leu Leu Asp Ala Gly  
 130 135 140

Thr Arg Xaa Gly Lys Asp Ser Ile Tyr His Leu Trp Lys Xaa Phe Asp  
 145 150 155 160

Val Asp Pro Met Cys Gly Gly Ala Cys Gly Glu Ile Lys Val Met Xaa  
 165 170 175

Ser His Gly Lys Lys Leu Leu Asn Pro Leu Val Ala Gly  
 180 185

<210> 48  
 <211> 2670

<212> DNA  
 <213> *Aspergillus fumigatus*

<220>  
 <221> CDS  
 <222> (1)..(2670)

```

<400> 48
atg ggc act cca agg ccc tat tcg gcg cat tca ccg cag gaa agc cga      48
Met Gly Thr Pro Arg Pro Tyr Ser Ala His Ser Pro Gln Glu Ser Arg
1                               5                               10                               15

agc agc ttc tac tcg cag ccc tcc caa tct cct aca cag cct acc tac      96
Ser Ser Phe Tyr Ser Gln Pro Ser Gln Ser Pro Thr Gln Pro Thr Tyr
20                               25                               30

ggt cgc gat gac gcg gaa gat caa caa caa tcc ctc ctt cga cgc agt     144
Gly Arg Asp Asp Ala Glu Asp Gln Gln Gln Ser Leu Leu Arg Arg Ser
35                               40                               45

tta gcc agt ccc aat ggc tgg tca tac gat gat ccc aac gta tct acc     192
Leu Ala Ser Pro Asn Gly Trp Ser Tyr Asp Asp Pro Asn Val Ser Thr
50                               55                               60

gac tct ctg agg cga tac aca ttg cat gat ccg ggg ata acc gca ttt     240
Asp Ser Leu Arg Arg Tyr Thr Leu His Asp Pro Gly Ile Thr Ala Phe
65                               70                               75                               80

gct ccc ccg tac ccg gag tcc gag gcc gcc gat gta cgc agc gca cgg     288
Ala Pro Pro Tyr Pro Glu Ser Glu Ala Ala Asp Val Arg Ser Ala Arg
85                               90                               95

atg tcg gga tac agt gga atc gag atg gat gcc tgg caa aga cga caa     336
Met Ser Gly Tyr Ser Gly Ile Glu Met Asp Ala Trp Gln Arg Arg Gln
100                              105                              110

ggg gtg aaa cca agt gcg cta cgg cga tat gga acc agg aag atc aac     384
Gly Val Lys Pro Ser Ala Leu Arg Arg Tyr Gly Thr Arg Lys Ile Asn
115                              120                              125

ctc gtc cag ggt tcg gta ctc agc gtt gac tac ccg gtg ccg agt gcg     432
Leu Val Gln Gly Ser Val Leu Ser Val Asp Tyr Pro Val Pro Ser Ala
130                              135                              140

att cag aac gcg atc cag gcg gag tat cgg gat gcg gag gaa gcg ttt     480
Ile Gln Asn Ala Ile Gln Ala Glu Tyr Arg Asp Ala Glu Glu Ala Phe
145                              150                              155                              160

cat gaa gaa ttc acg cat atg cgg tat act gcc gcc acc tgc gac cca     528
His Glu Glu Phe Thr His Met Arg Tyr Thr Ala Ala Thr Cys Asp Pro
165                              170                              175

gat gaa ttc act ctg cgc aac ggc tac aac cta cgt ccc gct atg tat     576
Asp Glu Phe Thr Leu Arg Asn Gly Tyr Asn Leu Arg Pro Ala Met Tyr
180                              185                              190

aac cgt cat acg gaa cgt ctc atc gcg atc act tat tat aat gag gat     624
Asn Arg His Thr Glu Arg Leu Ile Ala Ile Thr Tyr Tyr Asn Glu Asp
195                              200                              205

aaa gtt ctg acc gcc cga act ctg cat gga gtg atg caa aac gtc cgg     672

```

Lys	Val	Leu	Thr	Ala	Arg	Thr	Leu	His	Gly	Val	Met	Gln	Asn	Val	Arg		
210						215					220						
gac	att	gtg	aac	ctg	aag	aag	tca	gaa	ttt	tgg	aac	aag	gga	gga	ccg	720	
Asp	Ile	Val	Asn	Leu	Lys	Lys	Ser	Glu	Phe	Trp	Asn	Lys	Gly	Gly	Pro	240	
225					230					235							
gca	tgg	cag	aag	att	gtg	gtg	tgt	ctc	gtg	ttt	gat	gga	att	gag	cct	768	
Ala	Trp	Gln	Lys	Ile	Val	Val	Cys	Leu	Val	Phe	Asp	Gly	Ile	Glu	Pro	255	
				245					250								
tgc	gat	aag	aat	act	ctg	gat	gtc	ctc	gcc	acg	ata	ggt	gtg	tat	cag	816	
Cys	Asp	Lys	Asn	Thr	Leu	Asp	Val	Leu	Ala	Thr	Ile	Gly	Val	Tyr	Gln	270	
			260					265									
gat	ggg	gtg	atg	aaa	aaa	gat	gtg	gac	ggg	cgc	gag	aca	gtc	gca	cat	864	
Asp	Gly	Val	Met	Lys	Lys	Asp	Val	Asp	Gly	Arg	Glu	Thr	Val	Ala	His	285	
		275					280										
att	ttc	gag	tat	acg	aca	caa	tta	tcc	gtc	acc	ccg	aca	cag	cag	ctg	912	
Ile	Phe	Glu	Tyr	Thr	Thr	Gln	Leu	Ser	Val	Thr	Pro	Thr	Gln	Gln	Leu	300	
		290				295											
gtc	aga	ccg	cag	cct	aat	gat	cct	agc	aat	ctc	ccc	ccg	gtc	cag	atg	960	
Val	Arg	Pro	Gln	Pro	Asn	Asp	Pro	Ser	Asn	Leu	Pro	Pro	Val	Gln	Met	315	
305					310					315					320		
cta	ttc	tgc	ctc	aag	cag	aag	aac	agc	aag	aaa	atc	aat	tcc	cac	cgg	1008	
Leu	Phe	Cys	Leu	Lys	Gln	Lys	Asn	Ser	Lys	Lys	Ile	Asn	Ser	His	Arg	330	
				325					330					335			
tgg	ctg	ttc	aac	gcc	ttt	agt	cga	atc	ctg	aat	ccg	gaa	ata	tgc	atc	1056	
Trp	Leu	Phe	Asn	Ala	Phe	Ser	Arg	Ile	Leu	Asn	Pro	Glu	Ile	Cys	Ile	340	
			340					345					350				
ctg	ctt	gat	gct	ggc	acg	aag	ccc	ggg	agc	aaa	tcc	ttg	ctt	gcc	cta	1104	
Leu	Leu	Asp	Ala	Gly	Thr	Lys	Pro	Gly	Ser	Lys	Ser	Leu	Leu	Ala	Leu	355	
		355					360					365					
tgg	gaa	gca	ttc	tat	aat	gac	aaa	aca	ctg	ggc	gga	gca	tgc	ggc	gaa	1152	
Trp	Glu	Ala	Phe	Tyr	Asn	Asp	Lys	Thr	Leu	Gly	Gly	Ala	Cys	Gly	Glu	370	
		370				375					380						
atc	cat	gcc	atg	ctg	ggc	agg	ggg	tgg	cgc	aat	gtg	ctg	aac	cct	cta	1200	
Ile	His	Ala	Met	Leu	Gly	Arg	Gly	Trp	Arg	Asn	Val	Leu	Asn	Pro	Leu	385	
					390					395					400		
gtc	gca	gcg	cag	aat	ttt	gag	tac	aaa	att	tcc	aat	att	ctt	gat	aaa	1248	
Val	Ala	Ala	Gln	Asn	Phe	Glu	Tyr	Lys	Ile	Ser	Asn	Ile	Leu	Asp	Lys	405	
				405					410					415			
ccg	ctg	gaa	agc	gcc	ttt	ggc	tac	gtg	agt	gtg	cta	ccg	ggt	gct	ttc	1296	
Pro	Leu	Glu	Ser	Ala	Phe	Gly	Tyr	Val	Ser	Val	Leu	Pro	Gly	Ala	Phe	420	
			420					425					430				
tcg	gca	tat	cgc	tac	cgg	gcg	atc	atg	ggc	cga	ccg	ttg	gag	caa	tac	1344	
Ser	Ala	Tyr	Arg	Tyr	Arg	Ala	Ile	Met	Gly	Arg	Pro	Leu	Glu	Gln	Tyr	435	
		435					440					445					
ttt	cat	ggg	gat	cat	act	ttg	tcc	aag	cgg	ctg	gga	aag	aag	ggc	att	1392	
Phe	His	Gly	Asp	His	Thr	Leu	Ser	Lys	Arg	Leu	Gly	Lys	Lys	Gly	Ile	450	
		450				455					460						

gag ggg atg aat atc ttt aaa aag aac atg ttt ctt gca gag gat cgc Glu Gly Met Asn Ile Phe Lys Lys Asn Met Phe Leu Ala Glu Asp Arg 465 470 475 480	1440
atc cta tgc ttt gaa ctg gtg gcc aaa gct ggg tat aaa tgg cat ctc Ile Leu Cys Phe Glu Leu Val Ala Lys Ala Gly Tyr Lys Trp His Leu 485 490 495	1488
acg tat gtg aaa gca tcc aag gga gag aca gat gtt ccc gag gcg gcg Thr Tyr Val Lys Ala Ser Lys Gly Glu Thr Asp Val Pro Glu Ala Ala 500 505 510	1536
ccc gaa tac atc agt cag cgg cga cga tgg ctc aat ggc tcc ttt gct Pro Glu Tyr Ile Ser Gln Arg Arg Trp Leu Asn Gly Ser Phe Ala 515 520 525	1584
gcg agt ttg tat tcc atc atg cac ttc gga cgc atc tat aag agt ggt Ala Ser Leu Tyr Ser Ile Met His Phe Gly Arg Ile Tyr Lys Ser Gly 530 535 540	1632
cat agc ttc gtt cga atg ttc ttc ttg cat att cag atg att tac aac His Ser Phe Val Arg Met Phe Phe Leu His Ile Gln Met Ile Tyr Asn 545 550 555 560	1680
tgc tgc cag ctc atc atg acc tgg ttc tcg ttg gca tcc tac tgg ctg Cys Cys Gln Leu Ile Met Thr Trp Phe Ser Leu Ala Ser Tyr Trp Leu 565 570 575	1728
acc agc tcg gtc atc atg gac ctc gta ggg acg ccc agc tcg cat aac Thr Ser Ser Val Ile Met Asp Leu Val Gly Thr Pro Ser Ser His Asn 580 585 590	1776
aag tac aag gca tgg cca ttc ggc aac gat gcc tcc ccc att gtc aac Lys Tyr Lys Ala Trp Pro Phe Gly Asn Asp Ala Ser Pro Ile Val Asn 595 600 605	1824
ttt ttt gtc aaa tat ggt tat ctc ttg gtg ctg atg ctc caa ttt gtg Phe Phe Val Lys Tyr Gly Tyr Leu Leu Val Leu Met Leu Gln Phe Val 610 615 620	1872
ctg gct ctg gga aac cgc ccc aaa gcc tac acc atg tcg ttc ctc tgg Leu Ala Leu Gly Asn Arg Pro Lys Ala Tyr Thr Met Ser Phe Leu Trp 625 630 635 640	1920
ttt tct ctg gtg cag ttc tac gtg ctg atc ctg tcc ttc tac ctg gtc Phe Ser Leu Val Gln Phe Tyr Val Leu Ile Leu Ser Phe Tyr Leu Val 645 650 655	1968
gct aat gcc ttc atg ggt ggc atg atc gac ttt gat ttc gac caa ggc Ala Asn Ala Phe Met Gly Gly Met Ile Asp Phe Asp Phe Asp Gln Gly 660 665 670	2016
gtg ggc aac ttc ctc tcc tcc ttc ttc agc tcg act ggt gga ggg att Val Gly Asn Phe Leu Ser Ser Phe Phe Ser Ser Thr Gly Gly Gly Ile 675 680 685	2064
gtc ctg atc gcc ttg gtg tcc act tac ggc att tac att gtc gcg agc Val Leu Ile Ala Leu Val Ser Thr Tyr Gly Ile Tyr Ile Val Ala Ser 690 695 700	2112
att ctc tac atg gac cct tgg cac atc ctg acc agt tcc tgg gca tac Ile Leu Tyr Met Asp Pro Trp His Ile Leu Thr Ser Ser Trp Ala Tyr	2160

705	710	715	720	
ttc ctg ggc atg acc acg tcg atc aat att ctc atg gtg tat gcg ttc				2208
Phe Leu Gly Met Thr Thr Ser Ile Asn Ile Leu Met Val Tyr Ala Phe	725	730	735	
tgc aac tgg cac gat gtg tcg tgg ggt acg aag ggg tcc gat aag gcg				2256
Cys Asn Trp His Asp Val Ser Trp Gly Thr Lys Gly Ser Asp Lys Ala	740	745	750	
gac gct ctg ccc tca gcg cag acg aag aag gcc gac gcg agc aag agc				2304
Asp Ala Leu Pro Ser Ala Gln Thr Lys Lys Ala Asp Ala Ser Lys Ser	755	760	765	
aac ttc atc gag gag atc gat aaa ccg cag gca gac atc gac agc cag				2352
Asn Phe Ile Glu Glu Ile Asp Lys Pro Gln Ala Asp Ile Asp Ser Gln	770	775	780	
ttc gag gca acg gtc aaa cgg cgg ctg gcc ccg tat cag gag ccc aaa				2400
Phe Glu Ala Thr Val Lys Arg Arg Leu Ala Pro Tyr Gln Glu Pro Lys	785	790	800	
gaa gac tcg act atc agc ctg gat gat tcc tac cgc aac ttt cgg acc				2448
Glu Asp Ser Thr Ile Ser Leu Asp Asp Ser Tyr Arg Asn Phe Arg Thr	805	810	815	
agc ctg gtg ttg ctc tgg atc ttg agt aat ttg ctg gtc tct ctg ctc				2496
Ser Leu Val Leu Leu Trp Ile Leu Ser Asn Leu Leu Val Ser Leu Leu	820	825	830	
att acg agc gac ggc atc agg aag atg tgt ctg acg aac aca tcc aca				2544
Ile Thr Ser Asp Gly Ile Arg Lys Met Cys Leu Thr Asn Thr Ser Thr	835	840	845	
acg cgg acg cag tat tat ttc caa gtg att ttg tgg gcg aca gct gga				2592
Thr Arg Thr Gln Tyr Tyr Phe Gln Val Ile Leu Trp Ala Thr Ala Gly	850	855	860	
ctg tct atc ttc cga ttc att ggg tcg atc tac ttc ctg ggc aag tcg				2640
Leu Ser Ile Phe Arg Phe Ile Gly Ser Ile Tyr Phe Leu Gly Lys Ser	865	870	880	
gga atc tta tgt tgc gta acg cgt cga tga				2670
Gly Ile Leu Cys Cys Val Thr Arg Arg	885			

<210> 49  
 <211> 889  
 <212> PRT  
 <213> Aspergillus fumigatus

<400> 49

Met Gly Thr Pro Arg Pro Tyr Ser Ala His Ser Pro Gln Glu Ser Arg
1 5 10 15

Ser Ser Phe Tyr Ser Gln Pro Ser Gln Ser Pro Thr Gln Pro Thr Tyr
20 25 30

Gly Arg Asp Asp Ala Glu Asp Gln Gln Gln Ser Leu Leu Arg Arg Ser  
 35 40 45  
 Leu Ala Ser Pro Asn Gly Trp Ser Tyr Asp Asp Pro Asn Val Ser Thr  
 50 55 60  
 Asp Ser Leu Arg Arg Tyr Thr Leu His Asp Pro Gly Ile Thr Ala Phe  
 65 70 75 80  
 Ala Pro Pro Tyr Pro Glu Ser Glu Ala Ala Asp Val Arg Ser Ala Arg  
 85 90 95  
 Met Ser Gly Tyr Ser Gly Ile Glu Met Asp Ala Trp Gln Arg Arg Gln  
 100 105 110  
 Gly Val Lys Pro Ser Ala Leu Arg Arg Tyr Gly Thr Arg Lys Ile Asn  
 115 120 125  
 Leu Val Gln Gly Ser Val Leu Ser Val Asp Tyr Pro Val Pro Ser Ala  
 130 135 140  
 Ile Gln Asn Ala Ile Gln Ala Glu Tyr Arg Asp Ala Glu Glu Ala Phe  
 145 150 155 160  
 His Glu Glu Phe Thr His Met Arg Tyr Thr Ala Ala Thr Cys Asp Pro  
 165 170 175  
 Asp Glu Phe Thr Leu Arg Asn Gly Tyr Asn Leu Arg Pro Ala Met Tyr  
 180 185 190  
 Asn Arg His Thr Glu Arg Leu Ile Ala Ile Thr Tyr Tyr Asn Glu Asp  
 195 200 205  
 Lys Val Leu Thr Ala Arg Thr Leu His Gly Val Met Gln Asn Val Arg  
 210 215 220  
 Asp Ile Val Asn Leu Lys Lys Ser Glu Phe Trp Asn Lys Gly Gly Pro  
 225 230 235 240  
 Ala Trp Gln Lys Ile Val Val Cys Leu Val Phe Asp Gly Ile Glu Pro  
 245 250 255  
 Cys Asp Lys Asn Thr Leu Asp Val Leu Ala Thr Ile Gly Val Tyr Gln  
 260 265 270  
 Asp Gly Val Met Lys Lys Asp Val Asp Gly Arg Glu Thr Val Ala His  
 275 280 285

Ile Phe Glu Tyr Thr Thr Gln Leu Ser Val Thr Pro Thr Gln Gln Leu  
 290 295 300

Val Arg Pro Gln Pro Asn Asp Pro Ser Asn Leu Pro Pro Val Gln Met  
 305 310 315 320

Leu Phe Cys Leu Lys Gln Lys Asn Ser Lys Lys Ile Asn Ser His Arg  
 325 330 335

Trp Leu Phe Asn Ala Phe Ser Arg Ile Leu Asn Pro Glu Ile Cys Ile  
 340 345 350

Leu Leu Asp Ala Gly Thr Lys Pro Gly Ser Lys Ser Leu Leu Ala Leu  
 355 360 365

Trp Glu Ala Phe Tyr Asn Asp Lys Thr Leu Gly Gly Ala Cys Gly Glu  
 370 375 380

Ile His Ala Met Leu Gly Arg Gly Trp Arg Asn Val Leu Asn Pro Leu  
 385 390 395 400

Val Ala Ala Gln Asn Phe Glu Tyr Lys Ile Ser Asn Ile Leu Asp Lys  
 405 410 415

Pro Leu Glu Ser Ala Phe Gly Tyr Val Ser Val Leu Pro Gly Ala Phe  
 420 425 430

Ser Ala Tyr Arg Tyr Arg Ala Ile Met Gly Arg Pro Leu Glu Gln Tyr  
 435 440 445

Phe His Gly Asp His Thr Leu Ser Lys Arg Leu Gly Lys Lys Gly Ile  
 450 455 460

Glu Gly Met Asn Ile Phe Lys Lys Asn Met Phe Leu Ala Glu Asp Arg  
 465 470 475 480

Ile Leu Cys Phe Glu Leu Val Ala Lys Ala Gly Tyr Lys Trp His Leu  
 485 490 495

Thr Tyr Val Lys Ala Ser Lys Gly Glu Thr Asp Val Pro Glu Ala Ala  
 500 505 510

Pro Glu Tyr Ile Ser Gln Arg Arg Arg Trp Leu Asn Gly Ser Phe Ala  
 515 520 525

Ala Ser Leu Tyr Ser Ile Met His Phe Gly Arg Ile Tyr Lys Ser Gly

530					535					540					
His	Ser	Phe	Val	Arg	Met	Phe	Phe	Leu	His	Ile	Gln	Met	Ile	Tyr	Asn
545					550					555					560
Cys	Cys	Gln	Leu	Ile	Met	Thr	Trp	Phe	Ser	Leu	Ala	Ser	Tyr	Trp	Leu
				565					570					575	
Thr	Ser	Ser	Val	Ile	Met	Asp	Leu	Val	Gly	Thr	Pro	Ser	Ser	His	Asn
			580					585					590		
Lys	Tyr	Lys	Ala	Trp	Pro	Phe	Gly	Asn	Asp	Ala	Ser	Pro	Ile	Val	Asn
		595					600					605			
Phe	Phe	Val	Lys	Tyr	Gly	Tyr	Leu	Leu	Val	Leu	Met	Leu	Gln	Phe	Val
	610					615					620				
Leu	Ala	Leu	Gly	Asn	Arg	Pro	Lys	Ala	Tyr	Thr	Met	Ser	Phe	Leu	Trp
625					630					635					640
Phe	Ser	Leu	Val	Gln	Phe	Tyr	Val	Leu	Ile	Leu	Ser	Phe	Tyr	Leu	Val
				645					650					655	
Ala	Asn	Ala	Phe	Met	Gly	Gly	Met	Ile	Asp	Phe	Asp	Phe	Asp	Gln	Gly
			660					665					670		
Val	Gly	Asn	Phe	Leu	Ser	Ser	Phe	Phe	Ser	Ser	Thr	Gly	Gly	Gly	Ile
		675					680					685			
Val	Leu	Ile	Ala	Leu	Val	Ser	Thr	Tyr	Gly	Ile	Tyr	Ile	Val	Ala	Ser
	690					695					700				
Ile	Leu	Tyr	Met	Asp	Pro	Trp	His	Ile	Leu	Thr	Ser	Ser	Trp	Ala	Tyr
705					710					715					720
Phe	Leu	Gly	Met	Thr	Thr	Ser	Ile	Asn	Ile	Leu	Met	Val	Tyr	Ala	Phe
				725					730					735	
Cys	Asn	Trp	His	Asp	Val	Ser	Trp	Gly	Thr	Lys	Gly	Ser	Asp	Lys	Ala
			740					745					750		
Asp	Ala	Leu	Pro	Ser	Ala	Gln	Thr	Lys	Lys	Ala	Asp	Ala	Ser	Lys	Ser
		755					760					765			
Asn	Phe	Ile	Glu	Glu	Ile	Asp	Lys	Pro	Gln	Ala	Asp	Ile	Asp	Ser	Gln
	770					775					780				



Phe Glu Ala Thr Val Lys Arg Arg Leu Ala Pro Tyr Gln Glu Pro Lys  
785 790 795 800

Glu Asp Ser Thr Ile Ser Leu Asp Asp Ser Tyr Arg Asn Phe Arg Thr  
805 810 815

Ser Leu Val Leu Leu Trp Ile Leu Ser Asn Leu Leu Val Ser Leu Leu  
820 825 830

Ile Thr Ser Asp Gly Ile Arg Lys Met Cys Leu Thr Asn Thr Ser Thr  
835 840 845

Thr Arg Thr Gln Tyr Tyr Phe Gln Val Ile Leu Trp Ala Thr Ala Gly  
850 855 860

Leu Ser Ile Phe Arg Phe Ile Gly Ser Ile Tyr Phe Leu Gly Lys Ser  
865 870 875 880

Gly Ile Leu Cys Cys Val Thr Arg Arg  
885

<210> 50  
<211> 2751  
<212> DNA  
<213> Aspergillus oryzae

<220>  
<221> CDS  
<222> (1)..(2751)

<400> 50  
atg gcc tac caa ccg cct ggt aaa gat aat ggt gct cag tca cca aac 48  
Met Ala Tyr Gln Pro Pro Gly Lys Asp Asn Gly Ala Gln Ser Pro Asn  
1 5 10 15  
  
tac aac gat agc ggt cat cga ctg gaa gac ctg ccc cat ggc gcc act 96  
Tyr Asn Asp Ser Gly His Arg Leu Glu Asp Leu Pro His Gly Ala Thr  
20 25 30  
  
tat gaa gaa gaa gct tca aca gga ctg ctt tcc cac caa cag ggc ggt 144  
Tyr Glu Glu Glu Ala Ser Thr Gly Leu Leu Ser His Gln Gln Gly Gly  
35 40 45  
  
cct ttc ggt ggt cct ttc gac gac cct cat cag cgt ggc acc tcg cct 192  
Pro Phe Gly Gly Pro Phe Asp Asp Pro His Gln Arg Gly Thr Ser Pro  
50 55 60  
  
gtt cga cct acg tcg gga tac agc ttg act gaa aca tac gct ccg gac 240  
Val Arg Pro Thr Ser Gly Tyr Ser Leu Thr Glu Thr Tyr Ala Pro Asp  
65 70 75 80  
  
gcg ggt ttt cat gac cct tac agc acg acg ggc tcg gtt tac tcc ggc 288  
Ala Gly Phe His Asp Pro Tyr Ser Thr Thr Gly Ser Val Tyr Ser Gly  
85 90 95

aac tcg gca gaa aac ccc gcg gct gcc ttt ggc gtc ccg ggt cgt gta Asn Ser Ala Glu Asn Pro Ala Ala Phe Gly Val Pro Gly Arg Val 100 105 110	336
gct tct ccc tac gct cgc agt gaa aca tcc tcc aca gaa gca tgg cgc Ala Ser Pro Tyr Ala Arg Ser Glu Thr Ser Ser Thr Glu Ala Trp Arg 115 120 125	384
cag cgc cag gct cca gga ggt ggt ggc ggt ggt ggc ctc cgt cgt tac Gln Arg Gln Ala Pro Gly Gly Gly Gly Gly Gly Leu Arg Arg Tyr 130 135 140	432
gct acc aga aag gtc aag cta gtt cag ggt tcc gtc ctc agt gtc gat Ala Thr Arg Lys Val Lys Leu Val Gln Gly Ser Val Leu Ser Val Asp 145 150 155 160	480
tac ccc gtc ccc agt gct atc cag aat gcc atc caa gcc aag tac cgt Tyr Pro Val Pro Ser Ala Ile Gln Asn Ala Ile Gln Ala Lys Tyr Arg 165 170 175	528
aat gac ctg gag ggt ggc agc gag gag ttt acc cac atg cga tac acc Asn Asp Leu Glu Gly Gly Ser Glu Glu Phe Thr His Met Arg Tyr Thr 180 185 190	576
gct gcg aca tgt gat ccc aat gac ttc acc ctg cac aat ggt tac aat Ala Ala Thr Cys Asp Pro Asn Asp Phe Thr Leu His Asn Gly Tyr Asn 195 200 205	624
ctg cgt ccc gcc atg tat aac aga cac acc gag ttg ttg att gcg att Leu Arg Pro Ala Met Tyr Asn Arg His Thr Glu Leu Leu Ile Ala Ile 210 215 220	672
acc tat tat aac gaa gat aag acc ctt acc gct cgt acc ttg cac ggt Thr Tyr Tyr Asn Glu Asp Lys Thr Leu Thr Ala Arg Thr Leu His Gly 225 230 235 240	720
gtg atg cag aac att cgc gac att gtg aac ctc aag aag tcc gag ttc Val Met Gln Asn Ile Arg Asp Ile Val Asn Leu Lys Lys Ser Glu Phe 245 250 255	768
tgg aac aaa ggt gga ccc gcc tgg cag aaa att gtt gtc gct ctg gtc Trp Asn Lys Gly Gly Pro Ala Trp Gln Lys Ile Val Val Ala Leu Val 260 265 270	816
ttt gac ggt atc gat cct tgt gat aag gac act ttg gat gtc ctc gcc Phe Asp Gly Ile Asp Pro Cys Asp Lys Asp Thr Leu Asp Val Leu Ala 275 280 285	864
acc atc ggt atc tat cag gac ggt gtc atg aag cgt gac gtc gac ggc Thr Ile Gly Ile Tyr Gln Asp Gly Val Met Lys Arg Asp Val Asp Gly 290 295 300	912
aag gag acc gtg gct cat att ttc gaa tac acg acc caa ttg tcc gtg Lys Glu Thr Val Ala His Ile Phe Glu Tyr Thr Thr Gln Leu Ser Val 305 310 315 320	960
aca ccg aac cag caa ctc atc cgg ccc act gat gat ggc ccg acc acc Thr Pro Asn Gln Gln Leu Ile Arg Pro Thr Asp Asp Gly Pro Thr Thr 325 330 335	1008
ttg ccc ccg gtg cag atg atg ttc tgc tta aag cag aag aac agc aag Leu Pro Pro Val Gln Met Met Phe Cys Leu Lys Gln Lys Asn Ser Lys	1056

340										345					350					
aag atc aac tca cac aga tgg ctg ttc aat gcc ttc ggt cgt att ttg	1104																			
Lys Ile Asn Ser His Arg Trp Leu Phe Asn Ala Phe Gly Arg Ile Leu																				
355 360 365																				
aat cca gag gtt tgc atc ctt ctg gat gcc ggt act aag cct ggc cag	1152																			
Asn Pro Glu Val Cys Ile Leu Leu Asp Ala Gly Thr Lys Pro Gly Gln																				
370 375 380																				
aag tcc ctc ctg gcg ttg tgg gag ggc ttc tat aac gac aag gat ctg	1200																			
Lys Ser Leu Leu Ala Leu Trp Glu Gly Phe Tyr Asn Asp Lys Asp Leu																				
385 390 395 400																				
gga ggt gct tgt ggt gaa att cac gca atg ttg ggt aaa ggc tgg aag	1248																			
Gly Gly Ala Cys Gly Glu Ile His Ala Met Leu Gly Lys Gly Trp Lys																				
405 410 415																				
aat ctg atc aac ccc ctc gtc gcg gcc cag aac ttc gag tac aag atc	1296																			
Asn Leu Ile Asn Pro Leu Val Ala Ala Gln Asn Phe Glu Tyr Lys Ile																				
420 425 430																				
agt aat atc ctc gat aaa ccc ttg gag agt tct ttc ggt tat gtc agt	1344																			
Ser Asn Ile Leu Asp Lys Pro Leu Glu Ser Ser Phe Gly Tyr Val Ser																				
435 440 445																				
gtg ttg cct ggt gct ttc tcc gcc tat cgt ttc cgt gcc atc atg ggt	1392																			
Val Leu Pro Gly Ala Phe Ser Ala Tyr Arg Phe Arg Ala Ile Met Gly																				
450 455 460																				
cga ccc ctc gaa caa tat ttc cat ggt gat cac act ctc tca aaa cag	1440																			
Arg Pro Leu Glu Gln Tyr Phe His Gly Asp His Thr Leu Ser Lys Gln																				
465 470 475 480																				
ctg ggt aag aag ggt att gag ggc atg aac atc ttc aag aag aac atg	1488																			
Leu Gly Lys Lys Gly Ile Glu Gly Met Asn Ile Phe Lys Lys Asn Met																				
485 490 495																				
ttc ttg gcc gaa gat cgt atc ctt tgt ttc gaa ctg gtc gcc aag gct	1536																			
Phe Leu Ala Glu Asp Arg Ile Leu Cys Phe Glu Leu Val Ala Lys Ala																				
500 505 510																				
ggc tcc aaa tgg cac ttg tcc tac atc aaa gcc tcg aag ggt gaa act	1584																			
Gly Ser Lys Trp His Leu Ser Tyr Ile Lys Ala Ser Lys Gly Glu Thr																				
515 520 525																				
gac gtg ccg gaa ggt gtt gct gaa ttc att tcc cag cgt cgt cgt tgg	1632																			
Asp Val Pro Glu Gly Val Ala Glu Phe Ile Ser Gln Arg Arg Arg Trp																				
530 535 540																				
ttg aac ggt tct ttt gcg gcc ggt ctc tat tcg ctc atg cat ttc ggt	1680																			
Leu Asn Gly Ser Phe Ala Ala Gly Leu Tyr Ser Leu Met His Phe Gly																				
545 550 555 560																				
cgg atg tac aag agt gga cat aac atc atc cgt atg ttc ttc ttg cac	1728																			
Arg Met Tyr Lys Ser Gly His Asn Ile Ile Arg Met Phe Phe Leu His																				
565 570 575																				
att cag atg ttg tac aac gtt ttc aac act atc ctt aca tgg ttc tcc	1776																			
Ile Gln Met Leu Tyr Asn Val Phe Asn Thr Ile Leu Thr Trp Phe Ser																				
580 585 590																				

ctg gca tct tac tgg ttg acc acc acc gtc atc atg gac ttg gtc gga Leu Ala Ser Tyr Trp Leu Thr Thr Thr Val Ile Met Asp Leu Val Gly 595 600 605	1824
acg ccc agt gag agc aac ggt aac aaa gga ttc ccc ttc ggt aaa tcg Thr Pro Ser Glu Ser Asn Gly Asn Lys Gly Phe Pro Phe Gly Lys Ser 610 615 620	1872
gcg acc cct att atc aac aca att gtg aag tat gtc tac ctc gga ttg Ala Thr Pro Ile Ile Asn Thr Ile Val Lys Tyr Val Tyr Leu Gly Leu 625 630 635 640	1920
ttg ctc ttg cag ttc att ctc gct ctc ggt aac cgc ccc aag gga tcc Leu Leu Leu Gln Phe Ile Leu Ala Leu Gly Asn Arg Pro Lys Gly Ser 645 650 655	1968
cgc ttc tcg tac ctg aca tct ttc gtc gta ttc ggt atc att caa atc Arg Phe Ser Tyr Leu Thr Ser Phe Val Val Phe Gly Ile Ile Gln Ile 660 665 670	2016
tac gtt gtc gtc gac gct ctg tac ttg gtg gtt cgt gca ttc aca aac Tyr Val Val Val Asp Ala Leu Tyr Tyr Leu Val Val Arg Ala Phe Thr Asn 675 680 685	2064
agt gat gcg ata gat ttc gtc acc gat caa ggt gtt ggc gag ttc ctc Ser Asp Ala Ile Asp Phe Val Thr Asp Gln Gly Val Gly Glu Phe Leu 690 695 700	2112
aag tcg ttc ttc tcg tct tcc ggc gcc ggt atc att atc atc gcc ctg Lys Ser Phe Phe Ser Ser Ser Gly Ala Gly Ile Ile Ile Ile Ala Leu 705 710 715 720	2160
gct gct act ttc ggt ctc tac ttc gtc gct tcg ttc atg tac ctg gac Ala Ala Thr Phe Gly Leu Tyr Phe Val Ala Ser Phe Met Tyr Leu Asp 725 730 735	2208
cct tgg cat atg ttc acc tcg ttc ccc gcc tac atg ttc gtt cag tca Pro Trp His Met Phe Thr Ser Phe Pro Ala Tyr Met Phe Val Gln Ser 740 745 750	2256
tct tac atc aac gtt ctc aac gtg tac gcg ttc agc aac tgg cac gat Ser Tyr Ile Asn Val Leu Asn Val Tyr Ala Phe Ser Asn Trp His Asp 755 760 765	2304
gtc tcg tgg ggt acc aag ggt tct gat aag gcc gat gcg ctc cct tct Val Ser Trp Gly Thr Lys Ser Ser Asp Lys Ala Asp Ala Leu Pro Ser 770 775 780	2352
gca acg act acg aag gag gat ggc ggc aag gaa gct gtc att gag gaa Ala Thr Thr Thr Lys Glu Asp Gly Gly Lys Glu Ala Val Ile Glu Glu 785 790 795 800	2400
atc gac aag ccc cag gct gat att gac agc caa ttt gaa gcc act gtc Ile Asp Lys Pro Gln Ala Asp Ile Asp Ser Gln Phe Glu Ala Thr Val 805 810 815	2448
aag cgc gct ctc acc ccc tac gtc ccc cct gtg gag aag gat gag aag Lys Arg Ala Leu Thr Pro Tyr Val Pro Pro Val Glu Lys Asp Glu Lys 820 825 830	2496
tcc ttg gat gat tcc tac aag agt ttc cgt acc cgt ctt gtg acg ttg Ser Leu Asp Asp Ser Tyr Lys Ser Phe Arg Thr Arg Leu Val Thr Leu 835 840 845 850	2544

835	840	845	
tgg atc ttc agt aat gcc ttc ttg gct gta tgc att acc agt gac ggt			2592
Trp Ile Phe Ser Asn Ala Phe Leu Ala Val Cys Ile Thr Ser Asp Gly			
850	855	860	
atg gac aag ttt gga ttc acg aac acc gct acc gac cgt acg tcg cgt			2640
Met Asp Lys Phe Gly Phe Thr Asn Thr Ala Thr Asp Arg Thr Ser Arg			
865	870	875	880
ttc ttc cag gct ctc ctg tgg tcc aac gct gct gtc gca ctt gtc cgt			2688
Phe Phe Gln Ala Leu Leu Trp Ser Asn Ala Ala Val Ala Leu Val Arg			
	885	890	895
ttc att ggt gcc tgt tgg ttc ctg ggt aag acg ggt ctc atg tgc tgc			2736
Phe Ile Gly Ala Cys Trp Phe Leu Gly Lys Thr Gly Leu Met Cys Cys			
	900	905	910
ttc gct cgt cgg tag			2751
Phe Ala Arg Arg			
915			

<210> 51  
 <211> 916  
 <212> PRT  
 <213> Aspergillus oryzae

<400> 51

Met Ala Tyr Gln Pro Pro Gly Lys Asp Asn Gly Ala Gln Ser Pro Asn	
1 5 10 15	
Tyr Asn Asp Ser Gly His Arg Leu Glu Asp Leu Pro His Gly Ala Thr	
20 25 30	
Tyr Glu Glu Glu Ala Ser Thr Gly Leu Leu Ser His Gln Gln Gly Gly	
35 40 45	
Pro Phe Gly Gly Pro Phe Asp Asp Pro His Gln Arg Gly Thr Ser Pro	
50 55 60	
Val Arg Pro Thr Ser Gly Tyr Ser Leu Thr Glu Thr Tyr Ala Pro Asp	
65 70 75 80	
Ala Gly Phe His Asp Pro Tyr Ser Thr Thr Gly Ser Val Tyr Ser Gly	
85 90 95	
Asn Ser Ala Glu Asn Pro Ala Ala Ala Phe Gly Val Pro Gly Arg Val	
100 105 110	
Ala Ser Pro Tyr Ala Arg Ser Glu Thr Ser Ser Thr Glu Ala Trp Arg	
115 120 125	

Gln Arg Gln Ala Pro Gly Gly Gly Gly Gly Gly Gly Leu Arg Arg Tyr  
 130 135 140

Ala Thr Arg Lys Val Lys Leu Val Gln Gly Ser Val Leu Ser Val Asp  
 145 150 155 160

Tyr Pro Val Pro Ser Ala Ile Gln Asn Ala Ile Gln Ala Lys Tyr Arg  
 165 170 175

Asn Asp Leu Glu Gly Gly Ser Glu Glu Phe Thr His Met Arg Tyr Thr  
 180 185 190

Ala Ala Thr Cys Asp Pro Asn Asp Phe Thr Leu His Asn Gly Tyr Asn  
 195 200 205

Leu Arg Pro Ala Met Tyr Asn Arg His Thr Glu Leu Leu Ile Ala Ile  
 210 215 220

Thr Tyr Tyr Asn Glu Asp Lys Thr Leu Thr Ala Arg Thr Leu His Gly  
 225 230 235 240

Val Met Gln Asn Ile Arg Asp Ile Val Asn Leu Lys Lys Ser Glu Phe  
 245 250 255

Trp Asn Lys Gly Gly Pro Ala Trp Gln Lys Ile Val Val Ala Leu Val  
 260 265 270

Phe Asp Gly Ile Asp Pro Cys Asp Lys Asp Thr Leu Asp Val Leu Ala  
 275 280 285

Thr Ile Gly Ile Tyr Gln Asp Gly Val Met Lys Arg Asp Val Asp Gly  
 290 295 300

Lys Glu Thr Val Ala His Ile Phe Glu Tyr Thr Thr Gln Leu Ser Val  
 305 310 315 320

Thr Pro Asn Gln Gln Leu Ile Arg Pro Thr Asp Asp Gly Pro Thr Thr  
 325 330 335

Leu Pro Pro Val Gln Met Met Phe Cys Leu Lys Gln Lys Asn Ser Lys  
 340 345 350

Lys Ile Asn Ser His Arg Trp Leu Phe Asn Ala Phe Gly Arg Ile Leu  
 355 360 365

Asn Pro Glu Val Cys Ile Leu Leu Asp Ala Gly Thr Lys Pro Gly Gln  
 370 375 380

Lys Ser Leu Leu Ala Leu Trp Glu Gly Phe Tyr Asn Asp Lys Asp Leu  
 385 390 395 400

Gly Gly Ala Cys Gly Glu Ile His Ala Met Leu Gly Lys Gly Trp Lys  
 405 410 415

Asn Leu Ile Asn Pro Leu Val Ala Ala Gln Asn Phe Glu Tyr Lys Ile  
 420 425 430

Ser Asn Ile Leu Asp Lys Pro Leu Glu Ser Ser Phe Gly Tyr Val Ser  
 435 440 445

Val Leu Pro Gly Ala Phe Ser Ala Tyr Arg Phe Arg Ala Ile Met Gly  
 450 455 460

Arg Pro Leu Glu Gln Tyr Phe His Gly Asp His Thr Leu Ser Lys Gln  
 465 470 475 480

Leu Gly Lys Lys Gly Ile Glu Gly Met Asn Ile Phe Lys Lys Asn Met  
 485 490 495

Phe Leu Ala Glu Asp Arg Ile Leu Cys Phe Glu Leu Val Ala Lys Ala  
 500 505 510

Gly Ser Lys Trp His Leu Ser Tyr Ile Lys Ala Ser Lys Gly Glu Thr  
 515 520 525

Asp Val Pro Glu Gly Val Ala Glu Phe Ile Ser Gln Arg Arg Arg Trp  
 530 535 540

Leu Asn Gly Ser Phe Ala Ala Gly Leu Tyr Ser Leu Met His Phe Gly  
 545 550 555 560

Arg Met Tyr Lys Ser Gly His Asn Ile Ile Arg Met Phe Phe Leu His  
 565 570 575

Ile Gln Met Leu Tyr Asn Val Phe Asn Thr Ile Leu Thr Trp Phe Ser  
 580 585 590

Leu Ala Ser Tyr Trp Leu Thr Thr Thr Val Ile Met Asp Leu Val Gly  
 595 600 605

Thr Pro Ser Glu Ser Asn Gly Asn Lys Gly Phe Pro Phe Gly Lys Ser  
 610 615 620

Ala Thr Pro Ile Ile Asn Thr Ile Val Lys Tyr Val Tyr Leu Gly Leu

625		630		635		640									
Leu	Leu	Leu	Gln	Phe	Ile	Leu	Ala	Leu	Gly	Asn	Arg	Pro	Lys	Gly	Ser
				645					650					655	
Arg	Phe	Ser	Tyr	Leu	Thr	Ser	Phe	Val	Val	Phe	Gly	Ile	Ile	Gln	Ile
			660					665					670		
Tyr	Val	Val	Val	Asp	Ala	Leu	Tyr	Leu	Val	Val	Arg	Ala	Phe	Thr	Asn
		675					680					685			
Ser	Asp	Ala	Ile	Asp	Phe	Val	Thr	Asp	Gln	Gly	Val	Gly	Glu	Phe	Leu
	690					695					700				
Lys	Ser	Phe	Phe	Ser	Ser	Ser	Gly	Ala	Gly	Ile	Ile	Ile	Ile	Ala	Leu
705					710					715					720
Ala	Ala	Thr	Phe	Gly	Leu	Tyr	Phe	Val	Ala	Ser	Phe	Met	Tyr	Leu	Asp
				725					730					735	
Pro	Trp	His	Met	Phe	Thr	Ser	Phe	Pro	Ala	Tyr	Met	Phe	Val	Gln	Ser
			740					745					750		
Ser	Tyr	Ile	Asn	Val	Leu	Asn	Val	Tyr	Ala	Phe	Ser	Asn	Trp	His	Asp
		755					760					765			
Val	Ser	Trp	Gly	Thr	Lys	Gly	Ser	Asp	Lys	Ala	Asp	Ala	Leu	Pro	Ser
	770					775					780				
Ala	Thr	Thr	Thr	Lys	Glu	Asp	Gly	Gly	Lys	Glu	Ala	Val	Ile	Glu	Glu
785					790					795					800
Ile	Asp	Lys	Pro	Gln	Ala	Asp	Ile	Asp	Ser	Gln	Phe	Glu	Ala	Thr	Val
				805					810					815	
Lys	Arg	Ala	Leu	Thr	Pro	Tyr	Val	Pro	Pro	Val	Glu	Lys	Asp	Glu	Lys
			820					825					830		
Ser	Leu	Asp	Asp	Ser	Tyr	Lys	Ser	Phe	Arg	Thr	Arg	Leu	Val	Thr	Leu
		835					840					845			
Trp	Ile	Phe	Ser	Asn	Ala	Phe	Leu	Ala	Val	Cys	Ile	Thr	Ser	Asp	Gly
	850					855					860				
Met	Asp	Lys	Phe	Gly	Phe	Thr	Asn	Thr	Ala	Thr	Asp	Arg	Thr	Ser	Arg
865					870					875					880



Phe Phe Gln Ala Leu Leu Trp Ser Asn Ala Ala Val Ala Leu Val Arg  
885 890 895

Phe Ile Gly Ala Cys Trp Phe Leu Gly Lys Thr Gly Leu Met Cys Cys  
900 905 910

Phe Ala Arg Arg  
915

<210> 52  
<211> 1266  
<212> DNA  
<213> Mucor rouxii

<220>  
<221> CDS  
<222> (1)..(1266)

<400> 52  
atg caa atc aag aca ttc gcc ctt tca gct gca att gca caa gtt gct 48  
Met Gln Ile Lys Thr Phe Ala Leu Ser Ala Ala Ile Ala Gln Val Ala  
1 5 10 15  
act ctt gct tta gcc gac acc tcc gca aat tac tgg caa tca ttt act 96  
Thr Leu Ala Leu Ala Asp Thr Ser Ala Asn Tyr Trp Gln Ser Phe Thr  
20 25 30  
tct caa att aat ccc aag aac atc tcc att ccc tct att gag caa act 144  
Ser Gln Ile Asn Pro Lys Asn Ile Ser Ile Pro Ser Ile Glu Gln Thr  
35 40 45  
tca tcc att gac ccc act caa gaa tgt gct tac tac act cct gat gct 192  
Ser Ser Ile Asp Pro Thr Gln Glu Cys Ala Tyr Thr Pro Asp Ala  
50 55 60  
tca ttg ttc aca ttc aac gct tcc gaa tgg ccc tct atc tgg gaa gtc 240  
Ser Leu Phe Thr Phe Asn Ala Ser Glu Trp Pro Ser Ile Trp Glu Val  
65 70 75 80  
gct act acc aat ggt atg aat gag tct gcc gag ttc ctc agt gtc tac 288  
Ala Thr Thr Asn Gly Met Asn Glu Ser Ala Glu Phe Leu Ser Val Tyr  
85 90 95  
aat tct att gac tgg acc aag gca ccc aat att tct gtg cgt acc ctt 336  
Asn Ser Ile Asp Trp Thr Lys Ala Pro Asn Ile Ser Val Arg Thr Leu  
100 105 110  
gac gct aac ggc aac ttg gat acc act ggt tac aat act gct act gac 384  
Asp Ala Asn Gly Asn Leu Asp Thr Thr Gly Tyr Asn Thr Ala Thr Asp  
115 120 125  
cct gat tgt tgg tgg aca gct acc aca tgt acc tct ccc aag att tct 432  
Pro Asp Cys Trp Trp Thr Ala Thr Thr Cys Thr Ser Pro Lys Ile Ser  
130 135 140  
gat atc aat gac gat atc tcc aag tgt cct gaa ccc gag act tgg ggt 480  
Asp Ile Asn Asp Asp Ile Ser Lys Cys Pro Glu Pro Glu Thr Trp Gly  
145 150 155 160

ttg act tac gat gat gga cct aac tgc tct cac aac gct ttc tat gac Leu Thr Tyr Asp Asp Gly Pro Asn Cys Ser His Asn Ala Phe Tyr Asp 165 170 175	528
tac ctt caa gag caa aag ttg aag gcc tcc atg ttt tat att ggt tcc Tyr Leu Gln Glu Gln Lys Leu Lys Ala Ser Met Phe Tyr Ile Gly Ser 180 185 190	576
aat gtt gtt gac tgg cca tac ggt gct atg cgt ggt gtt gtt gat ggc Asn Val Val Asp Trp Pro Tyr Gly Ala Met Arg Gly Val Val Asp Gly 195 200 205	624
cat cac att gca tcc cac aca tgg tct cac cct caa atg aca acc aag His His Ile Ala Ser His Thr Trp Ser His Pro Gln Met Thr Thr Lys 210 215 220	672
acc aat caa gag gtc ctt gct gaa ttc tat tat act caa aag gcc atc Thr Asn Gln Glu Val Leu Ala Glu Phe Tyr Tyr Thr Gln Lys Ala Ile 225 230 235 240	720
aag ctc gct act ggt ttg acc cct cgt tac tgg cgt cct cct tat ggt Lys Leu Ala Thr Gly Leu Thr Pro Arg Tyr Trp Arg Pro Pro Tyr Gly 245 250 255	768
gat atc gat gat cgt gtt cgt tgg att gcc tct caa tta ggt tta act Asp Ile Asp Asp Arg Val Arg Trp Ile Ala Ser Gln Leu Gly Leu Thr 260 265 270	816
gct gtt att tgg aac ctc gat act gat gat tgg tct gct ggt gtc act Ala Val Ile Trp Asn Leu Asp Thr Asp Asp Trp Ser Ala Gly Val Thr 275 280 285	864
act act gtc gaa gct gtt gag caa agt tat tcc gat tat att gct atg Thr Thr Val Glu Ala Val Glu Gln Ser Tyr Ser Asp Tyr Ile Ala Met 290 295 300	912
ggt acc aat ggt act ttt gcc aac agt ggt aac att gta ttg acc cat Gly Thr Asn Gly Thr Phe Ala Asn Ser Gly Asn Ile Val Leu Thr His 305 310 315 320	960
gaa atc aac aca act atg agt ctc gct gtc gag aac ttg ccc aag atc Glu Ile Asn Thr Thr Met Ser Leu Ala Val Glu Asn Leu Pro Lys Ile 325 330 335	1008
att tct gcc tat aaa caa gtc atc gat gtc gct acc tgt tac aac att Ile Ser Ala Tyr Lys Gln Val Ile Asp Val Ala Thr Cys Tyr Asn Ile 340 345 350	1056
tct cac cct tac ttt gaa gac tac gaa tgg acc aat gtc ttg aac ggc Ser His Pro Tyr Phe Glu Asp Tyr Glu Trp Thr Asn Val Leu Asn Gly 355 360 365	1104
aca aaa tct tct gct acc gcc agt gga tct gct act tct gct agt gct Thr Lys Ser Ser Ala Thr Ala Ser Gly Ser Ala Thr Ser Ala Ser Ala 370 375 380	1152
tct gga ggc gct act acc gct gcc gct cat atc caa gct tct act agc Ser Gly Gly Ala Thr Thr Ala Ala His Ile Gln Ala Ser Thr Ser 385 390 395 400	1200
ggc gcc atg tct gtc ctt ccc aac ctc gcc ttg atc tct gcc ttc att Gly Ala Met Ser Val Leu Pro Asn Leu Ala Leu Ile Ser Ala Phe Ile	1248

405                      410                      415  
 gct acc ctg ttg ttt tag                      1266  
 Ala Thr Leu Leu Phe  
                     420  
  
 <210> 53  
 <211> 421  
 <212> PRT  
 <213> Mucor rouxii  
  
 <400> 53  
 Met Gln Ile Lys Thr Phe Ala Leu Ser Ala Ala Ile Ala Gln Val Ala  
 1                      5                      10                      15  
  
 Thr Leu Ala Leu Ala Asp Thr Ser Ala Asn Tyr Trp Gln Ser Phe Thr  
                     20                      25                      30  
  
 Ser Gln Ile Asn Pro Lys Asn Ile Ser Ile Pro Ser Ile Glu Gln Thr  
                     35                      40                      45  
  
 Ser Ser Ile Asp Pro Thr Gln Glu Cys Ala Tyr Tyr Thr Pro Asp Ala  
                     50                      55                      60  
  
 Ser Leu Phe Thr Phe Asn Ala Ser Glu Trp Pro Ser Ile Trp Glu Val  
 65                      70                      75                      80  
  
 Ala Thr Thr Asn Gly Met Asn Glu Ser Ala Glu Phe Leu Ser Val Tyr  
                     85                      90                      95  
  
 Asn Ser Ile Asp Trp Thr Lys Ala Pro Asn Ile Ser Val Arg Thr Leu  
                     100                      105                      110  
  
 Asp Ala Asn Gly Asn Leu Asp Thr Thr Gly Tyr Asn Thr Ala Thr Asp  
                     115                      120                      125  
  
 Pro Asp Cys Trp Trp Thr Ala Thr Thr Cys Thr Ser Pro Lys Ile Ser  
                     130                      135                      140  
  
 Asp Ile Asn Asp Asp Ile Ser Lys Cys Pro Glu Pro Glu Thr Trp Gly  
 145                      150                      155                      160  
  
 Leu Thr Tyr Asp Asp Gly Pro Asn Cys Ser His Asn Ala Phe Tyr Asp  
                     165                      170                      175  
  
 Tyr Leu Gln Glu Gln Lys Leu Lys Ala Ser Met Phe Tyr Ile Gly Ser  
                     180                      185                      190

Asn Val Val Asp Trp Pro Tyr Gly Ala Met Arg Gly Val Val Asp Gly  
 195 200 205

His His Ile Ala Ser His Thr Trp Ser His Pro Gln Met Thr Thr Lys  
 210 215 220

Thr Asn Gln Glu Val Leu Ala Glu Phe Tyr Tyr Thr Gln Lys Ala Ile  
 225 230 235 240

Lys Leu Ala Thr Gly Leu Thr Pro Arg Tyr Trp Arg Pro Pro Tyr Gly  
 245 250 255

Asp Ile Asp Asp Arg Val Arg Trp Ile Ala Ser Gln Leu Gly Leu Thr  
 260 265 270

Ala Val Ile Trp Asn Leu Asp Thr Asp Asp Trp Ser Ala Gly Val Thr  
 275 280 285

Thr Thr Val Glu Ala Val Glu Gln Ser Tyr Ser Asp Tyr Ile Ala Met  
 290 295 300

Gly Thr Asn Gly Thr Phe Ala Asn Ser Gly Asn Ile Val Leu Thr His  
 305 310 315 320

Glu Ile Asn Thr Thr Met Ser Leu Ala Val Glu Asn Leu Pro Lys Ile  
 325 330 335

Ile Ser Ala Tyr Lys Gln Val Ile Asp Val Ala Thr Cys Tyr Asn Ile  
 340 345 350

Ser His Pro Tyr Phe Glu Asp Tyr Glu Trp Thr Asn Val Leu Asn Gly  
 355 360 365

Thr Lys Ser Ser Ala Thr Ala Ser Gly Ser Ala Thr Ser Ala Ser Ala  
 370 375 380

Ser Gly Gly Ala Thr Thr Ala Ala Ala His Ile Gln Ala Ser Thr Ser  
 385 390 395 400

Gly Ala Met Ser Val Leu Pro Asn Leu Ala Leu Ile Ser Ala Phe Ile  
 405 410 415

Ala Thr Leu Leu Phe  
 420

<210> 54  
 <211> 1293

<212> DNA  
 <213> Gongronella butleri

<220>  
 <221> CDS  
 <222> (1)..(1293)

```

<400> 54
atg cgc cgc ctt gga cag ggc atc caa ttg gtg tcc gct gac tat tgg      48
Met Arg Arg Leu Gly Gln Gly Ile Gln Leu Val Ser Ala Asp Tyr Trp
1          5          10          15

tcc aac ttc aat tcg agc gtg aac cct ctc aac gtg aag gtg ccc caa      96
Ser Asn Phe Asn Ser Ser Val Asn Pro Leu Asn Val Lys Val Pro Gln
          20          25          30

atc aca cag cca cgt cga ttg atc acg tca cgg agt gca cgg tac tac      144
Ile Thr Gln Pro Arg Arg Leu Ile Thr Ser Arg Ser Ala Arg Tyr Tyr
          35          40          45

acg cct gat cca ctc gtt gat cac cat cac gcc cac cgg ctg ggg ccc      192
Thr Pro Asp Pro Leu Val Asp His His His Ala His Arg Leu Gly Pro
          50          55          60

aat tgg ctc acg gcc acc acc aat ggc atg aac acc agt gct gaa ttc      240
Asn Trp Leu Thr Ala Thr Thr Asn Gly Met Asn Thr Ser Ala Glu Phe
65          70          75          80

acc gcc ctt tac aac tcg atc aat tgg gac aac ggc ggc cca aac atc      288
Thr Ala Leu Tyr Asn Ser Ile Asn Trp Asp Asn Gly Gly Pro Asn Ile
          85          90          95

tcg gtg cgc acc ttc aac acc gat ggc tcc atg aac act aat ggc tac      336
Ser Val Arg Thr Phe Asn Thr Asp Gly Ser Met Asn Thr Asn Gly Tyr
          100          105          110

gac gtg gcc aat gat ccc gat tgt tgg tgg act gtc tct ggc tgc acg      384
Asp Val Ala Asn Asp Pro Asp Cys Trp Trp Thr Val Ser Gly Cys Thr
          115          120          125

gtg ccc aag ctc cag gat gtc aat gct gac att tac aag tgt cct gag      432
Val Pro Lys Leu Gln Asp Val Asn Ala Asp Ile Tyr Lys Cys Pro Glu
          130          135          140

ccc gat acg tgg ggc ttg ttc tat gac gac ggc ccc aat tgc tcg cac      480
Pro Asp Thr Trp Gly Leu Phe Tyr Asp Asp Gly Pro Asn Cys Ser His
145          150          155          160

aat gcc ttt tac aac ttt ttg cag gag caa aat ctg cgc gct tcc atg      528
Asn Ala Phe Tyr Asn Phe Leu Gln Glu Gln Asn Leu Arg Ala Ser Met
          165          170          175

ttt tac att ggt tcc aac gtc atg aac tgg ccc tat ggt gcc atg cgt      576
Phe Tyr Ile Gly Ser Asn Val Met Asn Trp Pro Tyr Gly Ala Met Arg
          180          185          190

ggt gtc caa gat ggc cat cac att gct ttc cac acc tgg tcc cat cag      624
Gly Val Gln Asp Gly His His Ile Ala Phe His Thr Trp Ser His Gln
          195          200          205

tca ttg acg acc ctg acg aac caa gaa ggg ctc gcc gag ttc tac tac      672

```

Ser	Leu	Thr	Thr	Leu	Thr	Asn	Gln	Glu	Gly	Leu	Ala	Glu	Phe	Tyr	Tyr		
210						215					220						
acg	caa	aag	atg	att	cac	ttg	gcc	act	ggt	gtg	aca	cct	cgc	tac	tgg	720	
Thr	Gln	Lys	Met	Ile	His	Leu	Ala	Thr	Gly	Val	Thr	Pro	Arg	Tyr	Trp	240	
225					230					235							
cgc	gct	ccc	tat	ggt	gat	gtc	gat	gat	cgt	gtg	cgc	tgg	att	gcc	acg	768	
Arg	Ala	Pro	Tyr	Gly	Asp	Val	Asp	Asp	Arg	Val	Arg	Trp	Ile	Ala	Thr	255	
				245					250					255			
caa	ttg	aac	ctg	acg	acg	atc	ctc	tgg	gac	tat	gat	acc	aac	gac	tgg	816	
Gln	Leu	Asn	Leu	Thr	Thr	Ile	Leu	Trp	Asp	Tyr	Asp	Thr	Asn	Asp	Trp	270	
			260					265					270				
cag	gca	ggc	gac	ggt	gtg	ccc	gag	tcc	acg	gtg	caa	aac	acg	tac	aat	864	
Gln	Ala	Gly	Asp	Gly	Val	Pro	Glu	Ser	Thr	Val	Gln	Asn	Thr	Tyr	Asn	285	
		275					280					285					
gaa	ttc	atc	cag	atg	ggc	aac	aat	ggt	tcg	atg	gcc	agc	ggt	ggc	aac	912	
Glu	Phe	Ile	Gln	Met	Gly	Asn	Asn	Gly	Ser	Met	Ala	Ser	Gly	Gly	Asn	300	
	290					295					300						
att	gta	ctg	acg	cac	gag	atc	aac	aac	acg	acg	atg	caa	ttg	gcc	gtc	960	
Ile	Val	Leu	Thr	His	Glu	Ile	Asn	Asn	Thr	Thr	Met	Gln	Leu	Ala	Val	320	
305					310					315							
gag	aac	atc	ccc	aac	atg	ctc	aag	tct	tac	aag	cac	gtc	gtc	aac	gtt	1008	
Glu	Asn	Ile	Pro	Asn	Met	Leu	Lys	Ser	Tyr	Lys	His	Val	Val	Asn	Val	335	
				325					330					335			
gcc	acc	tgc	atg	aac	atc	acg	ttc	ccg	aca	tgg	agc	aga	ccg	gtg	cct	1056	
Ala	Thr	Cys	Met	Asn	Ile	Thr	Phe	Pro	Thr	Trp	Ser	Arg	Pro	Val	Pro	350	
			340					345					350				
ttc	cct	tct	tta	gcc	aat	tta	ttg	cgc	aaa	aca	gct	tgg	gtg	cgg	gcg	1104	
Phe	Pro	Ser	Leu	Ala	Asn	Leu	Leu	Arg	Lys	Thr	Ala	Trp	Val	Arg	Ala	365	
		355					360					365					
gtg	ccg	cct	tca	aca	tta	cca	cgg	gcg	ccg	ggg	ctc	aga	gct	caa	gct	1152	
Val	Pro	Pro	Ser	Thr	Leu	Pro	Arg	Ala	Pro	Gly	Leu	Arg	Ala	Gln	Ala	380	
	370					375					380						
cgt	ttt	ctc	gtt	ggg	cgc	cat	gtc	ttt	gcc	caa	gcc	aat	gcc	ggt	gtc	1200	
Arg	Phe	Leu	Val	Gly	Arg	His	Val	Phe	Ala	Gln	Ala	Asn	Ala	Gly	Val	400	
385					390				395								
gcc	gtt	ttg	atg	aca	gtc	cgt	ggg	ccg	ttg	cgc	ttt	gca	ttt	aaa	tct	1248	
Ala	Val	Leu	Met	Thr	Val	Arg	Gly	Pro	Leu	Arg	Phe	Ala	Phe	Lys	Ser	415	
				405					410					415			
ttt	cca	atg	gga	ccc	cct	ttt	ctc	cct	tcc	tta	tat	gtt	ttt	tga		1293	
Phe	Pro	Met	Gly	Pro	Pro	Phe	Leu	Pro	Ser	Leu	Tyr	Val	Phe			430	
			420					425									

<210> 55  
 <211> 430  
 <212> PRT  
 <213> Gongronella butleri  
 <400> 55

Met Arg Arg Leu Gly Gln Gly Ile Gln Leu Val Ser Ala Asp Tyr Trp  
 1 5 10 15  
 Ser Asn Phe Asn Ser Ser Val Asn Pro Leu Asn Val Lys Val Pro Gln  
 20 25 30  
 Ile Thr Gln Pro Arg Arg Leu Ile Thr Ser Arg Ser Ala Arg Tyr Tyr  
 35 40 45  
 Thr Pro Asp Pro Leu Val Asp His His His Ala His Arg Leu Gly Pro  
 50 55 60  
 Asn Trp Leu Thr Ala Thr Thr Asn Gly Met Asn Thr Ser Ala Glu Phe  
 65 70 75 80  
 Thr Ala Leu Tyr Asn Ser Ile Asn Trp Asp Asn Gly Gly Pro Asn Ile  
 85 90 95  
 Ser Val Arg Thr Phe Asn Thr Asp Gly Ser Met Asn Thr Asn Gly Tyr  
 100 105 110  
 Asp Val Ala Asn Asp Pro Asp Cys Trp Trp Thr Val Ser Gly Cys Thr  
 115 120 125  
 Val Pro Lys Leu Gln Asp Val Asn Ala Asp Ile Tyr Lys Cys Pro Glu  
 130 135 140  
 Pro Asp Thr Trp Gly Leu Phe Tyr Asp Asp Gly Pro Asn Cys Ser His  
 145 150 155 160  
 Asn Ala Phe Tyr Asn Phe Leu Gln Glu Gln Asn Leu Arg Ala Ser Met  
 165 170 175  
 Phe Tyr Ile Gly Ser Asn Val Met Asn Trp Pro Tyr Gly Ala Met Arg  
 180 185 190  
 Gly Val Gln Asp Gly His His Ile Ala Phe His Thr Trp Ser His Gln  
 195 200 205  
 Ser Leu Thr Thr Leu Thr Asn Gln Glu Gly Leu Ala Glu Phe Tyr Tyr  
 210 215 220  
 Thr Gln Lys Met Ile His Leu Ala Thr Gly Val Thr Pro Arg Tyr Trp  
 225 230 235 240  
 Arg Ala Pro Tyr Gly Asp Val Asp Asp Arg Val Arg Trp Ile Ala Thr  
 245 250 255

Gln Leu Asn Leu Thr Thr Ile Leu Trp Asp Tyr Asp Thr Asn Asp Trp  
260 265 270

Gln Ala Gly Asp Gly Val Pro Glu Ser Thr Val Gln Asn Thr Tyr Asn  
275 280 285

Glu Phe Ile Gln Met Gly Asn Asn Gly Ser Met Ala Ser Gly Gly Asn  
290 295 300

Ile Val Leu Thr His Glu Ile Asn Asn Thr Thr Met Gln Leu Ala Val  
305 310 315 320

Glu Asn Ile Pro Asn Met Leu Lys Ser Tyr Lys His Val Val Asn Val  
325 330 335

Ala Thr Cys Met Asn Ile Thr Phe Pro Thr Trp Ser Arg Pro Val Pro  
340 345 350

Phe Pro Ser Leu Ala Asn Leu Leu Arg Lys Thr Ala Trp Val Arg Ala  
355 360 365

Val Pro Pro Ser Thr Leu Pro Arg Ala Pro Gly Leu Arg Ala Gln Ala  
370 375 380

Arg Phe Leu Val Gly Arg His Val Phe Ala Gln Ala Asn Ala Gly Val  
385 390 395 400

Ala Val Leu Met Thr Val Arg Gly Pro Leu Arg Phe Ala Phe Lys Ser  
405 410 415

Phe Pro Met Gly Pro Pro Phe Leu Pro Ser Leu Tyr Val Phe  
420 425 430

<210> 56  
<211> 1689  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)..(1689)

<400> 56  
atg tca ctc ctt tac atc att ctt cta ttc aca caa ttc tta cta ctg 48  
Met Ser Leu Leu Tyr Ile Ile Leu Leu Phe Thr Gln Phe Leu Leu Leu  
1 5 10 15

cca acc gat gcc ttt gat agg tct gct aac aca aat att gct gtt tat 96  
Pro Thr Asp Ala Phe Asp Arg Ser Ala Asn Thr Asn Ile Ala Val Tyr



20	25	30	
tgg ggt caa aac tca gca gga acg caa gaa tcc tta gct act tac tgt Trp Gly Gln Asn Ser Ala Gly Thr Gln Glu Ser Leu Ala Thr Tyr Cys 35 40 45			144
gaa tct tct gat gct gat att ttc cta tta tct ttc ttg aac caa ttt Glu Ser Ser Asp Ala Asp Ile Phe Leu Leu Ser Phe Leu Asn Gln Phe 50 55 60			192
cca acc ctt ggt ttg aac ttt gcc aac gca tgc tct gat act ttt tct Pro Thr Leu Gly Leu Asn Phe Ala Asn Ala Cys Ser Asp Thr Phe Ser 65 70 75 80			240
gat ggc tta ctt cac tgc acc cag att gct gaa gat att gaa act tgc Asp Gly Leu Leu His Cys Thr Gln Ile Ala Glu Asp Ile Glu Thr Cys 85 90 95			288
cag tcc cta gga aag aaa gtt cta tta tca tta ggt ggt gca tct ggt Gln Ser Leu Gly Lys Lys Val Leu Leu Ser Leu Gly Gly Ala Ser Gly 100 105 110			336
agc tac ctc ttt tca gat gat tct caa gcg gaa act ttt gca caa act Ser Tyr Leu Phe Ser Asp Asp Ser Gln Ala Glu Thr Phe Ala Gln Thr 115 120 125			384
tta tgg gat act ttc ggt gaa ggt aca ggt gcc agt gag aga cca ttt Leu Trp Asp Thr Phe Gly Glu Gly Thr Gly Ala Ser Glu Arg Pro Phe 130 135 140			432
gac tca gca gtc gtt gat ggt ttt gat ttt gat att gaa aac aac aac Asp Ser Ala Val Val Asp Gly Phe Asp Phe Asp Ile Glu Asn Asn Asn 145 150 155 160			480
gaa gta ggc tat agt gcg tta cgt acc aag tta aga act ttg ttt gcc Glu Val Gly Tyr Ser Ala Leu Arg Thr Lys Leu Arg Thr Leu Phe Ala 165 170 175			528
gaa ggt aca aag caa tat tac ctt tct gcc gca cca caa tgt cca tac Glu Gly Thr Lys Gln Tyr Tyr Leu Ser Ala Ala Pro Gln Cys Pro Tyr 180 185 190			576
ccg gat gct tct gtt ggt gac ttg ttg gaa aat gca gac att gat ttt Pro Asp Ala Ser Val Gly Asp Leu Leu Glu Asn Ala Asp Ile Asp Phe 195 200 205			624
gcg ttc atc caa ttt tac aat aat tac tgc agt gtg agt ggt caa ttc Ala Phe Ile Gln Phe Tyr Asn Asn Tyr Cys Ser Val Ser Gly Gln Phe 210 215 220			672
aat tgg gat act tgg tta acc tat gct caa act gta tcc cca aat aaa Asn Trp Asp Thr Trp Leu Thr Tyr Ala Gln Thr Val Ser Pro Asn Lys 225 230 235 240			720
aat atc aaa ctg ttc tta ggt tta cct ggt tct gct tct gct gct ggc Asn Ile Lys Leu Phe Leu Gly Leu Pro Gly Ser Ala Ser Ala Ala Gly 245 250 255			768
tct ggt tat att tct gac act tct tta ttg gaa tca act att gca gat Ser Gly Tyr Ile Ser Asp Thr Ser Leu Leu Glu Ser Thr Ile Ala Asp 260 265 270			816

att gcc tct tca agt tct ttt ggt ggt att gcg tta tgg gat gca tct Ile Ala Ser Ser Ser Ser Phe Gly Gly Ile Ala Leu Trp Asp Ala Ser 275 280 285	864
caa gcc ttt tcc aac gag cta aat ggt gaa cca tat gtt gag att ttg Gln Ala Phe Ser Asn Glu Leu Asn Gly Glu Pro Tyr Val Glu Ile Leu 290 295 300	912
aag aat ttg cta aca agt gct agc cag acc gcc act act aca gtt gcc Lys Asn Leu Leu Thr Ser Ala Ser Gln Thr Ala Thr Thr Thr Val Ala 305 310 315 320	960
acc tca aaa acc tca gca gcc tca act tca tct gct tca act tca tct Thr Ser Lys Thr Ser Ala Ala Ser Thr Ser Ser Ala Ser Thr Ser Ser 325 330 335	1008
gct tca act tct cag aaa aag acc aca caa tct acg aca tct aca caa Ala Ser Thr Ser Gln Lys Lys Thr Thr Gln Ser Thr Thr Ser Thr Gln 340 345 350	1056
agt aaa agc aaa gtt act tta tct cca act gca agc agc gct atc aaa Ser Lys Ser Lys Val Thr Leu Ser Pro Thr Ala Ser Ser Ala Ile Lys 355 360 365	1104
aca tca att act caa act aca aaa aca ttg acg agt agc acc aag aca Thr Ser Ile Thr Gln Thr Thr Lys Thr Leu Thr Ser Ser Thr Lys Thr 370 375 380	1152
aaa tct agt cta ggt acc acc aca aca gag agc act tta aat tca gtt Lys Ser Ser Leu Gly Thr Thr Thr Glu Ser Thr Leu Asn Ser Val 385 390 395 400	1200
gct atc aca agt atg aaa act act cta tct tcc caa ata acc agt gct Ala Ile Thr Ser Met Lys Thr Thr Leu Ser Ser Gln Ile Thr Ser Ala 405 410 415	1248
gcc ttg gtg acc cct caa aca act act act agc ata gtt tct tcg gcc Ala Leu Val Thr Pro Gln Thr Thr Thr Ser Ile Val Ser Ser Ala 420 425 430	1296
cca att caa aca gct atc act agt act ctt tcg cca gca acg aag agt Pro Ile Gln Thr Ala Ile Thr Ser Thr Leu Ser Pro Ala Thr Lys Ser 435 440 445	1344
tct tct gtc gtt tcc cta cag aca gct act act agt acg ctt tcc cca Ser Ser Val Val Ser Leu Gln Thr Ala Thr Thr Ser Thr Leu Ser Pro 450 455 460	1392
aca acg acc agt aca agc tca ggt agt aca agc tca ggt agt aca agc Thr Thr Thr Ser Thr Ser Ser Gly Ser Thr Ser Ser Gly Ser Thr Ser 465 470 475 480	1440
tca gac agt aca gct cgt aca ttg gct aaa gaa ttg aat gct caa tat Ser Asp Ser Thr Ala Arg Thr Leu Ala Lys Glu Leu Asn Ala Gln Tyr 485 490 495	1488
gcg gct ggt aaa ttg aac ggt aaa tct acc tgt act gaa ggt gaa att Ala Ala Gly Lys Leu Asn Gly Lys Ser Thr Cys Thr Glu Gly Glu Ile 500 505 510	1536
gca tgc tct gct gat ggg aag ttc gcc gtt tgt gat cat agc gct tgg Ala Cys Ser Ala Asp Gly Lys Phe Ala Val Cys Asp His Ser Ala Trp	1584

515	520	525	
gtt tac atg gaa tgt gct tct gga acc aca tgt tat gct tat gac tcc			1632
Val Tyr Met Glu Cys Ala Ser Gly Thr Thr Cys Tyr Ala Tyr Asp Ser			
530	535	540	
ggc gac tca gtc tat acc caa tgt aat ttc tct tat ttg gaa agc aat			1680
Gly Asp Ser Val Tyr Thr Gln Cys Asn Phe Ser Tyr Leu Glu Ser Asn			
545	550	555	560
tac ttt taa			1689
Tyr Phe			

<210> 57  
 <211> 562  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 57

Met Ser Leu Leu Tyr Ile Ile Leu Leu Phe Thr Gln Phe Leu Leu Leu
1 5 10 15

Pro Thr Asp Ala Phe Asp Arg Ser Ala Asn Thr Asn Ile Ala Val Tyr
20 25 30

Trp Gly Gln Asn Ser Ala Gly Thr Gln Glu Ser Leu Ala Thr Tyr Cys
35 40 45

Glu Ser Ser Asp Ala Asp Ile Phe Leu Leu Ser Phe Leu Asn Gln Phe
50 55 60

Pro Thr Leu Gly Leu Asn Phe Ala Asn Ala Cys Ser Asp Thr Phe Ser
65 70 75 80

Asp Gly Leu Leu His Cys Thr Gln Ile Ala Glu Asp Ile Glu Thr Cys
85 90 95

Gln Ser Leu Gly Lys Lys Val Leu Leu Ser Leu Gly Gly Ala Ser Gly
100 105 110

Ser Tyr Leu Phe Ser Asp Asp Ser Gln Ala Glu Thr Phe Ala Gln Thr
115 120 125

Leu Trp Asp Thr Phe Gly Glu Gly Thr Gly Ala Ser Glu Arg Pro Phe
130 135 140

Asp Ser Ala Val Val Asp Gly Phe Asp Phe Asp Ile Glu Asn Asn Asn
145 150 155 160

Glu Val Gly Tyr Ser Ala Leu Arg Thr Lys Leu Arg Thr Leu Phe Ala  
 165 170 175

Glu Gly Thr Lys Gln Tyr Tyr Leu Ser Ala Ala Pro Gln Cys Pro Tyr  
 180 185 190

Pro Asp Ala Ser Val Gly Asp Leu Leu Glu Asn Ala Asp Ile Asp Phe  
 195 200 205

Ala Phe Ile Gln Phe Tyr Asn Asn Tyr Cys Ser Val Ser Gly Gln Phe  
 210 215 220

Asn Trp Asp Thr Trp Leu Thr Tyr Ala Gln Thr Val Ser Pro Asn Lys  
 225 230 235 240

Asn Ile Lys Leu Phe Leu Gly Leu Pro Gly Ser Ala Ser Ala Ala Gly  
 245 250 255

Ser Gly Tyr Ile Ser Asp Thr Ser Leu Leu Glu Ser Thr Ile Ala Asp  
 260 265 270

Ile Ala Ser Ser Ser Ser Phe Gly Gly Ile Ala Leu Trp Asp Ala Ser  
 275 280 285

Gln Ala Phe Ser Asn Glu Leu Asn Gly Glu Pro Tyr Val Glu Ile Leu  
 290 295 300

Lys Asn Leu Leu Thr Ser Ala Ser Gln Thr Ala Thr Thr Thr Val Ala  
 305 310 315 320

Thr Ser Lys Thr Ser Ala Ala Ser Thr Ser Ser Ala Ser Thr Ser Ser  
 325 330 335

Ala Ser Thr Ser Gln Lys Lys Thr Thr Gln Ser Thr Thr Ser Thr Gln  
 340 345 350

Ser Lys Ser Lys Val Thr Leu Ser Pro Thr Ala Ser Ser Ala Ile Lys  
 355 360 365

Thr Ser Ile Thr Gln Thr Thr Lys Thr Leu Thr Ser Ser Thr Lys Thr  
 370 375 380

Lys Ser Ser Leu Gly Thr Thr Thr Thr Glu Ser Thr Leu Asn Ser Val  
 385 390 395 400

Ala Ile Thr Ser Met Lys Thr Thr Leu Ser Ser Gln Ile Thr Ser Ala  
 405 410 415

Ala Leu Val Thr Pro Gln Thr Thr Thr Thr Ser Ile Val Ser Ser Ala  
420 425 430

Pro Ile Gln Thr Ala Ile Thr Ser Thr Leu Ser Pro Ala Thr Lys Ser  
435 440 445

Ser Ser Val Val Ser Leu Gln Thr Ala Thr Thr Ser Thr Leu Ser Pro  
450 455 460

Thr Thr Thr Ser Thr Ser Ser Gly Ser Thr Ser Ser Gly Ser Thr Ser  
465 470 475 480

Ser Asp Ser Thr Ala Arg Thr Leu Ala Lys Glu Leu Asn Ala Gln Tyr  
485 490 495

Ala Ala Gly Lys Leu Asn Gly Lys Ser Thr Cys Thr Glu Gly Glu Ile  
500 505 510

Ala Cys Ser Ala Asp Gly Lys Phe Ala Val Cys Asp His Ser Ala Trp  
515 520 525

Val Tyr Met Glu Cys Ala Ser Gly Thr Thr Cys Tyr Ala Tyr Asp Ser  
530 535 540

Gly Asp Ser Val Tyr Thr Gln Cys Asn Phe Ser Tyr Leu Glu Ser Asn  
545 550 555 560

Tyr Phe

<210> 58  
<211> 837  
<212> DNA  
<213> Nocardioiodes sp.

<220>  
<221> CDS  
<222> (1)..(837)

<400> 58  
atg cgt ctc aag cac ccc acc gcc cgg ctc gcc ctc gcc gcc ctg ctg 48  
Met Arg Leu Lys His Pro Thr Ala Arg Leu Ala Leu Ala Leu Leu  
1 5 10 15

gtc gcc gtc ccg cgc agt gtc gcg gcc gcc ggc acc gtc cac gcc gcc 96  
Val Ala Val Pro Arg Ser Val Ala Ala Ala Gly Thr Val His Ala Ala  
20 25 30

ccg gcc ccc gcc ggc gcc acc cgg ctc gcg gcc gtc ggg ctg gac gac 144  
Pro Ala Pro Ala Gly Ala Thr Arg Leu Ala Ala Val Gly Leu Asp Asp

35	40	45	
ccg cac aag aag gac atc gcc atg cag ctg gtg tcc agc gcc gag aac Pro His Lys Lys Asp Ile Ala Met Gln Leu Val Ser Ser Ala Glu Asn 50 55 60			192
tcc tcc ctc gac tgg aag tcc cag tac aag tac atc gag gac atc aag Ser Ser Leu Asp Trp Lys Ser Gln Tyr Lys Tyr Ile Glu Asp Ile Lys 65 70 75 80			240
gac ggc cgc ggc tac acc gcc ggc atc atc ggc ttc tgt tcc ggc acc Asp Gly Arg Gly Tyr Thr Ala Gly Ile Ile Gly Phe Cys Ser Gly Thr 85 90 95			288
ggc gac atg ctc gac ctg gtc gca gac tac acc gac ctc aag ccg ggc Gly Asp Met Leu Asp Leu Val Ala Asp Tyr Thr Asp Leu Lys Pro Gly 100 105 110			336
aac atc ctc gcc aag tac ctc ccg gcg ctg cgc aag gtc aac ggc acc Asn Ile Leu Ala Lys Tyr Leu Pro Ala Leu Arg Lys Val Asn Gly Thr 115 120 125			384
gag tcg cac gcc ggc ctc gcg tcc gcc ttc gag aag gac tgg gcc acc Glu Ser His Ala Gly Leu Ala Ser Ala Phe Glu Lys Asp Trp Ala Thr 130 135 140			432
gcc gcc aag gac agc gtc ttc cag cag gcc cag aac gac gag cgc gac Ala Ala Lys Asp Ser Val Phe Gln Gln Ala Gln Asn Asp Glu Arg Asp 145 150 155 160			480
cgc tcg tac ttc aac ccc gcg gtc aac cag gcc aag gcg agc ctg cgc Arg Ser Tyr Phe Asn Pro Ala Val Asn Gln Ala Lys Ala Ser Leu Arg 165 170 175			528
gcg ctc ggc cag ttc gcc tac tac gac gcg atc gtc atg cac ggc ccc Ala Leu Gly Gln Phe Ala Tyr Tyr Asp Ala Ile Val Met His Gly Pro 180 185 190			576
ggc gac agc tcg gac agc ttc ggc ggc atc cgc aag gcc gcc atg aag Gly Asp Ser Ser Asp Ser Phe Gly Gly Ile Arg Lys Ala Ala Met Lys 195 200 205			624
aag gcc aag acc ccc gcc cag ggc cgc gac gag gcc acc tac ctc aag Lys Ala Lys Thr Pro Ala Gln Gly Arg Asp Glu Ala Thr Tyr Leu Lys 210 215 220			672
gcc ttc ctg gcg gcc cgc aag acc gtg atg ctg aag gag gag gcc cac Ala Phe Leu Ala Ala Arg Lys Thr Val Met Leu Lys Glu Glu Ala His 225 230 235 240			720
tcg gac acc agc cgg gtc gac acc gag cag acg gtg ttc ctc aac gcc Ser Asp Thr Ser Arg Val Asp Thr Glu Gln Thr Val Phe Leu Asn Ala 245 250 255			768
aag aac ttc gac ctc aac ccg ccg ctg aag tgg aag gtc tac ggg gac Lys Asn Phe Asp Leu Asn Pro Pro Leu Lys Trp Lys Val Tyr Gly Asp 260 265 270			816
agc tac gcc atc aac agc tga Ser Tyr Ala Ile Asn Ser 275			837

<210> 59  
 <211> 278  
 <212> PRT  
 <213> Nocardiooides sp.

<400> 59

Met Arg Leu Lys His Pro Thr Ala Arg Leu Ala Leu Ala Ala Leu Leu  
 1 5 10 15

Val Ala Val Pro Arg Ser Val Ala Ala Gly Thr Val His Ala Ala  
 20 25 30

Pro Ala Pro Ala Gly Ala Thr Arg Leu Ala Ala Val Gly Leu Asp Asp  
 35 40 45

Pro His Lys Lys Asp Ile Ala Met Gln Leu Val Ser Ser Ala Glu Asn  
 50 55 60

Ser Ser Leu Asp Trp Lys Ser Gln Tyr Lys Tyr Ile Glu Asp Ile Lys  
 65 70 75 80

Asp Gly Arg Gly Tyr Thr Ala Gly Ile Ile Gly Phe Cys Ser Gly Thr  
 85 90 95

Gly Asp Met Leu Asp Leu Val Ala Asp Tyr Thr Asp Leu Lys Pro Gly  
 100 105 110

Asn Ile Leu Ala Lys Tyr Leu Pro Ala Leu Arg Lys Val Asn Gly Thr  
 115 120 125

Glu Ser His Ala Gly Leu Ala Ser Ala Phe Glu Lys Asp Trp Ala Thr  
 130 135 140

Ala Ala Lys Asp Ser Val Phe Gln Gln Ala Gln Asn Asp Glu Arg Asp  
 145 150 155 160

Arg Ser Tyr Phe Asn Pro Ala Val Asn Gln Ala Lys Ala Ser Leu Arg  
 165 170 175

Ala Leu Gly Gln Phe Ala Tyr Tyr Asp Ala Ile Val Met His Gly Pro  
 180 185 190

Gly Asp Ser Ser Asp Ser Phe Gly Gly Ile Arg Lys Ala Ala Met Lys  
 195 200 205

Lys Ala Lys Thr Pro Ala Gln Gly Arg Asp Glu Ala Thr Tyr Leu Lys  
 210 215 220

Ala Phe Leu Ala Ala Arg Lys Thr Val Met Leu Lys Glu Glu Ala His  
225 230 235 240

Ser Asp Thr Ser Arg Val Asp Thr Glu Gln Thr Val Phe Leu Asn Ala  
245 250 255

Lys Asn Phe Asp Leu Asn Pro Pro Leu Lys Trp Lys Val Tyr Gly Asp  
260 265 270

Ser Tyr Ala Ile Asn Ser  
275